

Protein Sequence Searches - February 2005

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- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 06:12:05 ; Search time 22 Seconds
(without alignments)
291.810 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVCGAGTCCA.....CSRFPDGRYRCGMDLKNINF 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	105	4 US-09-712-529-5	Sequence 5, Appl
2	498	100.0	105	4 US-10-212-201A-5	Sequence 5, Appl
3	498	100.0	105	4 US-10-212-355-5	Sequence 5, Appl
4	486	97.6	105	4 US-09-621-976-5350	Sequence 5350, Ap
5	357	71.7	80	4 US-09-513-999C-4698	Sequence 4698, Ap
6	291	58.4	108	4 US-09-712-529-2	Sequence 2, Appl
7	291	58.4	108	4 US-10-212-201A-2	Sequence 2, Appl
8	291	58.4	108	4 US-10-212-355-2	Sequence 2, Appl
9	107.5	21.6	224	3 US-09-161-241-14	Sequence 14, Appl
10	102	20.5	186	4 US-09-949-016-7146	Sequence 7146, Ap
11	102	20.5	207	3 US-09-161-241-13	Sequence 13, Appl
12	102	20.5	259	3 US-09-161-241-12	Sequence 12, Appl
13	102	20.5	259	4 US-09-949-016-6872	Sequence 6872, Ap
14	101	20.3	259	3 US-09-161-241-11	Sequence 11, Appl
15	100.5	20.2	350	3 US-09-161-241-9	Sequence 9, Appl
16	100.5	20.2	350	4 US-09-907-794A-236	Sequence 236, App
17	100.5	20.2	350	4 US-09-905-125A-236	Sequence 236, App
18	100.5	20.2	350	4 US-09-902-775A-236	Sequence 236, App
19	100.5	20.2	350	4 US-09-906-700-236	Sequence 236, App
20	100.5	20.2	350	4 US-09-903-603A-236	Sequence 236, App
21	100.5	20.2	350	4 US-09-904-820A-236	Sequence 236, App
22	100.5	20.2	350	4 US-09-909-064-236	Sequence 236, App
23	100.5	20.2	350	4 US-09-905-81A-236	Sequence 236, App
24	100.5	20.2	350	4 US-09-906-618-236	Sequence 236, App
25	100.5	20.2	375	4 US-09-949-016-7856	Sequence 7856, Ap
26	100.5	20.2	375	4 US-09-949-016-7857	Sequence 7857, Ap
27	100.5	20.2	375	4 US-09-949-016-7858	Sequence 7858, Ap

28	98.5	19.8	349	3 US-09-161-241-8	Sequence 8, Appl
29	97	19.5	266	4 US-09-161-241-10	Sequence 10, Appl
30	97	19.5	266	4 US-09-976-594-1086	Sequence 1086, Ap
31	81	16.3	1964	3 US-09-467-997-1	Sequence 1, Appl
32	76.5	15.4	1342	4 US-09-561-709B-13	Sequence 13, Appl
33	73	14.7	124	4 US-09-949-016-11293	Sequence 11293, A
34	72.5	14.6	163	2 US-08-219-237B-5	Sequence 5, Appl
35	72.5	14.6	163	3 US-08-477-347-13	Sequence 13, Appl
36	72.5	14.6	163	3 US-08-476-862-4	Sequence 4, Appl
37	72.5	14.6	163	3 US-08-468-560C-5	Sequence 5, Appl
38	72.5	14.6	163	4 US-08-828-683A-13	Sequence 13, Appl
39	72.5	14.6	163	4 US-09-800-909-4	Sequence 4, Appl
40	72.5	14.6	163	4 US-09-800-908-13	Sequence 13, Appl
41	72.5	14.6	163	4 US-09-823-323-54	Sequence 54, Appl
42	72.5	14.6	164	2 US-08-232-087A-9	Sequence 9, Appl
43	72.5	14.6	227	3 US-08-974-022-48	Sequence 48, Appl
44	72.5	14.6	227	3 US-08-795-445A-48	Sequence 48, Appl
45	72.5	14.6	227	3 US-08-795-447A-48	Sequence 48, Appl

ALIGNMENTS

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RESULT 1
US-09-712-529-5
; Sequence 5, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-5

Query Match      100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AVITGACERDVCGAGTCCAISLMLRGLRMCPPLGRBEGEGHPSHKKVFPFRKKHHTCP 60
      |||
DB      20 AVITGACERDVCGAGTCCAISLMLRGLRMCTPLGRBEGEGHPSHKKVFPFRKKHHTCP 79

QY      61 CLPNILCSRFPDGRYRCGMDLKNINF 86
      |||
DB      80 CLPNILCSRFPDGRYRCGMDLKNINF 105

RESULT 2
US-10-212-201A-5
; Sequence 5, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-201A-5
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Query Match          100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AVITGACERDVQCGAGTCCCAISLMLRGLRMCTPLGREGECHPSHKVPPFRKKHHTCP 60
    |||
DB 20 AVITGACERDVQCGAGTCCCAISLMLRGLRMCTPLGREGECHPSHKVPPFRKKHHTCP 79
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QY 61 CLPNLCSRPPDGRYRCMDLKNINF 86
    |||
DB 80 CLPNLCSRPPDGRYRCMDLKNINF 105
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RESULT 3

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US-10-212-355-5
; Sequence 5, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-355-5
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Query Match          100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||
DB 20 AVITGACERDVQCGAGTCCCAISLMLRGLRMCTPLGREGECHPSHKVPPFRKKHHTCP 79
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QY 61 CLPNLCSRPPDGRYRCMDLKNINF 86
    |||
DB 80 CLPNLCSRPPDGRYRCMDLKNINF 105
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RESULT 4

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US-09-621-976-5350
; Sequence 5350, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5350
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
FEATURE:
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; NAME/KEY: SIGNAL
; LOCATION: -19..-1
; NAME/KEY: UNSURE
; LOCATION: 38
; OTHER INFORMATION: Xaa = Ala, Gly
US-09-621-976-5350
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Query Match          97.6%; Score 486; DB 4; Length 105;
Best Local Similarity 96.5%; Pred. No. 9.4e-50;
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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DB 20 AVITGACERDVQCGAGTCCCAISLMLRGLRMCTPLGREGECHPSHKVPPFRKKHHTCP 79
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QY 61 CLPNLCSRPPDGRYRCMDLKNINF 86
    |||
DB 80 CLPNLCSRPPDGRYRCMDLKNINF 105
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RESULT 5

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US-09-513-999C-4698
; Sequence 4698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4698
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19..-1
; OTHER INFORMATION: score 7.2
US-09-513-999C-4698
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Query Match          71.7%; Score 357; DB 4; Length 80;
Best Local Similarity 98.4%; Pred. No. 1e-34;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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    |||
DB 20 AVITGACERDVQCGAGTCCCAISLMLRGLRMCTPLGREGECHPSHKVPPFRKKHHTCP 79
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QY 61 C 61
    |||
DB 80 C 80
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RESULT 6

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US-09-712-529-2
; Sequence 2, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
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; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-712-529-2

Query Match
Best Local Similarity 58.4%; Score 291; DB 4; Length 108;
Matches 45; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMLRGLMCTPLGRGEGECHPSGHKVPFPRKRKHTCP 60
DB 28 AVITGACDSDSCGGGMCACAVSIWKSIRICTPMGKLDSDCHPLTRKVPFGRMHHTCP 87
QY 61 CLPNLLCSRFPPDGRYRC 77
DB 88 CLPGLACLRITSPFRFIC 104

RESULT 7
US-10-212-201A-2
; Sequence 2, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-212-201A-2

Query Match
Best Local Similarity 58.4%; Score 291; DB 4; Length 108;
Matches 45; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMLRGLMCTPLGRGEGECHPSGHKVPFPRKRKHTCP 60
DB 28 AVITGACDSDSCGGGMCACAVSIWKSIRICTPMGKLDSDCHPLTRKVPFGRMHHTCP 87
QY 61 CLPNLLCSRFPPDGRYRC 77
DB 88 CLPGLACLRITSPFRFIC 104

RESULT 8
US-10-212-355-2
; Sequence 2, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-212-355-2

Query Match
Best Local Similarity 58.4%; Score 291; DB 4; Length 108;
Matches 45; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMLRGLMCTPLGRGEGECHPSGHKVPFPRKRKHTCP 60
DB 28 AVITGACDSDSCGGGMCACAVSIWKSIRICTPMGKLDSDCHPLTRKVPFGRMHHTCP 87
QY 61 CLPNLLCSRFPPDGRYRC 77
DB 88 CLPGLACLRITSPFRFIC 104

RESULT 9
US-09-161-241-14
; Sequence 14, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Deguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 224
; TYPE: PRF
; ORGANISM: Human
US-09-161-241-14

Query Match
Best Local Similarity 21.6%; Score 107.5; DB 3; Length 224;
Matches 22; Conservative 5; Mismatches 32; Indels 3; Gaps 1;

QY 6 ACERDVCGAGTCCATSLMLRGLMCTPLGRGEGECHPSGHKVPFPRKRKHTCP 65
DB 144 SCLRTFDGCGPGLCARHFW--TKICKVLLGGVCSRRGHKDTAQAPEIFORCDGPG 200
QY 66 LC 67
DB 201 LC 202

RESULT 10
US-09-949-016-7146
; Sequence 7146, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7146
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LENGTH: 186
TYPE: PRT
ORGANISM: Human
US-09-949-016-7146

Query Match 20.5%; Score 102; DB 4; Length 186;
Best Local Similarity 31.5%; Pred. No. 0.00026;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

Db 7 CERDVCGAGTCCASIMLRGLMCTPLGRGEECC---HPGSHKVPFPRKRKHTCPCL 62
110 CLRSSDCIEGFCARHFW---TKICKPVHGGVCTKQRKKGSHGLEIFOR-----CDCA 161

QY 63 PNLCGRFPDGRY 75
Db 162 KGLSCRWKDATY 174

RESULT 11
US-09-161-241-13
Sequence 13, Application US/09161241
Patent No. 6344541

GENERAL INFORMATION:
APPLICANT: Baas, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13

LENGTH: 207
TYPE: PRT
ORGANISM: Human
US-09-161-241-13

Query Match 20.5%; Score 102; DB 3; Length 207;
Best Local Similarity 31.5%; Pred. No. 0.00029;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 7 CERDVCGAGTCCASIMLRGLMCTPLGRGEECC---HPGSHKVPFPRKRKHTCPCL 62
Db 131 CLRSSDCIEGFCARHFW---TKICKPVHGGVCTKQRKKGSHGLEIFOR-----CDCA 162

QY 63 PNLCGRFPDGRY 75
Db 183 KGLSCRWKDATY 195

RESULT 12
US-09-161-241-12
Sequence 12, Application US/09161241
Patent No. 6344541

GENERAL INFORMATION:
APPLICANT: Baas, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12

LENGTH: 259
TYPE: PRT
ORGANISM: Human
US-09-161-241-12

Query Match 20.5%; Score 102; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.00037;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 7 CERDVCGAGTCCASIMLRGLMCTPLGRGEECC---HPGSHKVPFPRKRKHTCPCL 62
Db 183 CLRSSDCIEGFCARHFW---TKICKPVHGGVCTKQRKKGSHGLEIFOR-----CDCA 234

QY 63 PNLCGRFPDGRY 75
Db 235 KGLSCRWKDATY 247

RESULT 13
US-09-949-016-6872
Sequence 6872, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6872

LENGTH: 259
TYPE: PRT
ORGANISM: Human
US-09-949-016-6872

Query Match 20.5%; Score 102; DB 4; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.00037;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 7 CERDVCGAGTCCASIMLRGLMCTPLGRGEECC---HPGSHKVPFPRKRKHTCPCL 62
Db 183 CLRSSDCIEGFCARHFW---TKICKPVHGGVCTKQRKKGSHGLEIFOR-----CDCA 234

QY 63 PNLCGRFPDGRY 75
Db 235 KGLSCRWKDATY 247

RESULT 14
US-09-161-241-11
Sequence 11, Application US/09161241
Patent No. 6344541

GENERAL INFORMATION:
APPLICANT: Baas, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11

LENGTH: 259
TYPE: PRT
ORGANISM: Mouse
US-09-161-241-11

Query Match 20.3%; Score 101; DB 3; Length 259;

Best Local Similarity 31.5%; Pred. No. 0.00049;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3

QY 7 CERDQAGAGTCCATLMLRGLRMCTPLRGREGEC-----HPGSHKVPFFRKRRKHTNCPL 62
Db 183 CLRSSDIDGFCARHFW---TKICKPLVHQGEVCTQRRKKGSHGLIFQ-----CDCA 234

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Oy      63  PNLCSRFPPDGRY  75
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Db      235 KGLSCVKWKDATY  247

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RESULT 15

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US-09-161-241-9
: Sequence 9, Application US/09161241
: Patent No. 6344541
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: GENERAL INFORMATION:
:
: APPLICANT: Bass, Michael B
: APPLICANT: Sullivan, John K
: APPLICANT: Theill, Lars E
: APPLICANT: Wang, Daqiang
:
: TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
:
: FILE REFERENCE: A-548
:
: CURRENT APPLICATION NUMBER: US/09/161,241
: CURRENT FILING DATE: 1998-09-25
:
: NUMBER OF SEQ ID NOS: 78
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 9
:
: LENGTH: 350
:
: TYPE: prt
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: ORGANISM: Human
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US-09-161-241-9

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Query Match	20.2%	Score 100.5;	DB 3;	Length 350;
Best Local Similarity	37.7%;	Pred. No. 0.00078;		
Matches	26;	Conservative	3;	Mismatches 29;
			Indels	11;
			Gaps	4;

QY / CERDVQCGAGTCCCAISLMLRGI--RMTPLRGEGEECH-PGSLKVPFFRRKKI-----HT 58
 : | | | | | : | | | | | :
 DB 208 CDNGRDCQPGILCAFG--RGLLPVCTPLPYEGELCHDPA SRLDLITWELRPGALDR 264

QY 59 CPCLPNLTC 67
|||
Db 265 CPCASGLTC 273
|||

Search completed: May 16, 2005, 06:34:54
Job time : 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 06:36:12 ; Search time 38 Seconds
(without alignments)
217.754 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498
Sequence: 1 AVITGACERDVOCAGACTCCA.....CSRFPDGRYRCMDLKNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 29189

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.5	12.3	83	2 T26545	hypothetical prote
2	58	11.6	46	2 A44794	antimicrobial pept
3	54.5	10.9	57	2 C46554	growth modulatory
4	54	10.8	63	2 S08572	chymotrypsin/elast
5	53.5	10.7	57	2 A46554	growth modulatory
6	53	10.6	47	2 B58319	gamma-zetathionin 2
7	53	10.6	77	2 S29563	endothelin 2 precu
8	52.5	10.5	70	2 A55824	drosomycin precurs
9	52	10.4	77	2 S47158	metallochionein II
10	51.5	10.3	77	2 AF2564	hypothetical prote
11	51	10.2	84	2 JN0469	85K MRK-20 recogni
12	50.5	10.1	47	2 S69145	gamma-chinin Str-a
13	49.5	9.9	61	2 C81079	hypothetical prote
14	49.5	9.9	74	2 S05594	pseudochitonin St1
15	49	9.8	62	2 I51538	metallochionein -
16	49	9.8	65	2 S03858	carboxypeptidase A
17	49	9.8	67	2 PC4008	hypothetical prote
18	49	9.8	72	2 A42325	orf 5' to pheC - p
19	48.5	9.7	54	1 S23075	protein PMP-DI - m
20	48.5	9.7	79	2 T06381	proteinase inhibit
21	48	9.6	66	2 S59621	metallochionein is
22	48	9.6	67	2 B69830	hypothetical prote
23	48	9.6	74	2 AF3436	hypothetical prote
24	47.5	9.5	64	2 A25775	metallochionein A
25	47.5	9.5	65	1 NTS83C	neurotoxin 3 - bar
26	46.5	9.3	58	1 A00841	hypothetical prote
27	46.5	9.3	65	1 NTSR1C	neurotoxin 1 - bar
28	46	9.2	43	2 JC2554	holotricin 1 - Hol
29	46	9.2	44	2 I48942	cellular disintegr

30	46	9.2	48	2 S68952	omega-hordochionin
31	46	9.2	60	2 B27490	metallochionein B
32	46	9.2	60	2 A83099	hypothetical prote
33	46	9.2	62	2 H81791	hypothetical prote
34	46	9.2	66	2 A55869	crustacean-specific
35	46	9.2	81	4 B49316	hypothetical prote
36	45.5	9.1	48	2 S13963	alpha-amyase inh
37	45.5	9.1	66	1 NTSR2C	neurotoxin 2 - bar
38	45.5	9.1	72	2 T00612	hypothetical prote
39	45.5	9.1	72	2 I50022	Sry-related sequen
40	45.5	9.1	72	2 I50023	Sry-related sequen
41	45.5	9.1	73	2 B86279	Fl4L17.22 protein
42	45.5	9.1	81	2 S27366	metallochionein B
43	45.5	9.1	81	2 S27369	metallochionein B
44	45.5	9.1	84	2 F87306	conserved hypothet
45	45	9.0	49	2 I48946	cellular disintegr

ALIGNMENTS

RESULT 1

T26545 hypothetical protein Y1A5A.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26545

R:Barlow, K.

A:Submitted to the EMBL Data Library, January 1998

A:Reference number: Z20228

A:Accession: T26545

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-83 <MTL>

A:Cross-references: UNIPROT:Q9XHT6; EMBL:AL021177; PIDN:CAA15979.1; GSPDB:GN00021; CESP

A:Experimental source: clone Y1A5A

C:Genetic:

A:Gene: CESP:Y1A5A.2

A:Map position: 3

A:Introns: 27/2

Query Match

Best Local Similarity 37.5%; Pred. No. 13;

Matches 18; Conservative 1; Mismatches 10; Indels 19; Gaps 3;

QY 17 TCCTAISLWIRGLMCTPLGRBGECHP-GSHKVPFRKXHTTCECLP 63

DB 48 TCCCTSL-----GASAPTRSPRPV---RKQHTAPSP 77

RESULT 2

A44794 antimicrobial peptide eMAP-1 - horse (fragment)

C:Species: Equus caballus (domestic horse)

C:Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A44794; A40833

R:Conuto, M.A.; Harwig, S.S.; Cullor, J.S.; Hughes, J.P.; Lehrer, R.I.

Infect. Immun. 60, 3065-3071, 1992

A:Title: Identification of eMAP-1, an antimicrobial peptide from equine neutrophils.

A:Reference number: A44794; MUID:92347972; PMID:1639474

A:Accession: A44794

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-46 <COU>

A:Cross-references: UNIPROT:P80930

A:Experimental source: neutrophils

A>Note: sequence extracted from NCBI backbone (NCBI:109730)

C:Superfamily: granulin

Query Match

Best Local Similarity 33.3%; Pred. No. 18;

Matches 17; Conservative 3; Mismatches 23; Indels 8; Gaps 2;

A:Experimental source: seeds
 A>Note: this is a revision to the sequence from reference S13931
 R:Biochem. 223, 135-139, 1994
 A:Title: Pseudochonin-St1, a potato peptide active against potato pathogens.
 A:Reference number: S45659; MUID:94307252; PMID:8033886
 A:Accession: S45659
 A:Molecule type: protein
 A:Residues: 28, 'N', 30-47 <MOR>
 A:Experimental source: strain cv. Desiree
 C:Superfamily: gamma-thionin
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-74/Product: pseudochonin St1 #status experimental <MAT>

Query Match 9.9%; Score 49.5; DB 2; Length 74;
 Best Local Similarity 26.3%; Pred. No. 2.1e+02;
 Matches 15; Conservative 3; Mismatches 16; Indels 21; Gaps 2;

Db 39 GPCRDSNCAS-----VCETERPSGNCCHG-----FRRCPCPC 74

RESULT 15
 151538
 metallothionein - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: 151538
 R:Saint-Jacques, E.; Seguin, C.
 DNA Cell Biol. 12, 329-340, 1993
 A:Title: Cloning and nucleotide sequence of a complementary DNA encoding Xenopus laevis
 A:Reference number: 151538; MUID:93263990; PMID:8494609
 A:Accession: 151538
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-62 <SH1>
 A:Cross-references: UNIPROT:Q05890; GB:M96729; NID:g214585; PIND:AAB5949.1; PID:g21458
 C:Superfamily: metallothionein

Query Match 9.8%; Score 49; DB 2; Length 62;
 Best Local Similarity 26.7%; Pred. No. 2e+02;
 Matches 16; Conservative 4; Mismatches 28; Indels 12; Gaps 3;

Db 8 CERDVGSGTTCGSCNCKCTCKSCGCCP--ACSKCSQCHCKSKK-----CSC 60

Search completed: May 16, 2005, 06:53:16
 Job time : 40 secs

Query Match 9.9%; Score 49.5; DB 2; Length 61;
 Best Local Similarity 28.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 4; Mismatches 26; Indels 11; Gaps 3;

Db 9 RDVOCGAGTCCAISL-----LWGLRMCTPLGRGEGCHPS--HKVFFRKXKH 57

RESULT 14
 S05594
 pseudochonin St1 precursor - potato (strain cv. Bintje)
 C:Species: Solanum tuberosum (potato)
 A:Variety: strain cv. Bintje
 C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
 C:Accession: S05594; S45659
 R:Stiekema, W.D.; Heidekamp, F.; Dirkse, W.G.; van Beckum, J.; de Haan, P.; ten Bosch, C.
 Plant Mol. Biol. 11, 255-269, 1988
 A:Title: Molecular cloning and analysis of four potato tuber mRNAs.
 A:Reference number: S05592
 A:Accession: S05594
 A:Molecule type: mRNA
 A:Residues: 1-74 <ST1>
 A:Cross-references: UNIPROT:P20346; EMBL:X13180; NID:g21393; PIND:CAA31577.1; PID:g21394
 A:Experimental source: strain cv. Bintje
 A>Note: it is unknown whether 1-Met is the initiator or whether translation is initiated
 A>Note: the authors designated this protein as proteinase inhibitor (Bowman Birk) homoid

Query Match 10.1%; Score 50.5; DB 2; Length 47;
 Best Local Similarity 35.7%; Pred. No. 1.1e+02;
 Matches 10; Conservative 4; Mismatches 5; Indels 9; Gaps 1;

Db 41 CHPGSHKVPFFRRKHHTCCPLNLLCS 68

RESULT 13
 C81079
 hypothetical protein NMB1477 [imported] - Neisseria meningitidis (strain MC58 serogroup
 C:Species: Neisseria meningitidis
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: C81079
 R:Rettelin, H.; Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Halt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scarlata, V.; Maignani, V.; Pizze, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappapoli, R.; Va
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307
 A:Accession: C81079
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-61 <TET>
 A:Cross-references: UNIPROT:Q9JY04; GB:AE002497; GB:AE002098; NID:g7226712; PIND:AAF4183
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB1477

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OM protein - protein search, using sw model

Run on: May 16, 2005, 06:35:46 ; Search time 173 Seconds
(without alignments)
254,560 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCSDMKKNF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 188592

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432	86.7	81	2	Q8K457 mus musculus
2	310.5	86.3	81	2	VPRA_DENPO
3	73	14.7	64	1	TX16_PHORI
4	70	14.1	68	1	TX16_PHONI
5	66	13.3	85	1	HEPC_MORCS
6	63.5	12.8	70	1	CX2X_CONBE
7	61.5	12.3	83	2	Q9XXT6
8	58.5	11.7	50	2	Q64DV8
9	58.5	11.7	76	2	Q64AE9
10	58	11.6	46	1	ENAL_HORSE
11	57.5	11.5	68	1	ACTX_HADVE
12	56	11.2	78	1	MT2_MUSAC
13	55.5	11.1	57	2	Q9PEN7
14	55.5	11.1	76	2	Q7UW0
15	55.5	11.1	80	2	Q96S92
16	55	11.0	49	2	Q8H6K2
17	54.5	10.9	57	1	GRN3_CYPCA
18	54.5	10.8	72	1	LCR3_ARATH
19	54	10.8	78	2	Q8TB48
20	54	10.8	75	1	LC20_ARATH
21	54	10.8	75	2	Q8K4W3
22	53.5	10.7	57	1	GRN1_CYPCA
23	53.5	10.7	60	1	MTA_CYP51
24	53.5	10.7	60	2	Q7IDA0
25	53.5	10.7	63	2	Q7ORL9
26	53	10.6	47	1	S1A1_SORBI
27	53	10.6	47	1	THZ2_MAIZE
28	53	10.6	67	2	Q7NG77
29	52.5	10.5	68	1	MT_LYTP1
30	52.5	10.5	70	1	DMYC_DROME
31	52.5	10.5	75	1	LCR6_ARATH

32	52.5	10.5	86	2	Q7AN55	Q7AN55 nanoarchaeu
33	52	10.4	60	2	Q8MSH6	Q8MSH6 dirosophila
34	52	10.4	65	1	ICB2_ASCSU	P07852 ascaris suu
35	52	10.4	76	1	EC_MAIZE	P43401 zea mays (m
36	52	10.4	84	1	SC9_CENSC	O95WC9 centuroide
37	51.5	10.3	48	2	Q6RUW5	Q6RUW5 carassius c
38	51.5	10.3	59	1	R3J3_ENTPA	Q83E10 entecococu
39	51.5	10.3	67	2	Q96717	Q96717 fucus vesic
40	51.5	10.3	74	2	Q8WQ95	Q8WQ95 ciassostrea
41	51.5	10.3	77	2	Q75WH3	Q75WH3 macrothele
42	51.5	10.3	77	2	Q8YK17	Q8YK17 anabaena ap
43	51.5	10.3	78	2	Q9MB66	Q9MB66 nicotiana t
44	51.5	10.3	85	2	Q8FA94	Q8FA94 escherichia
45	51	10.2	73	2	Q86RB8	Q86RB8 trypanosoma

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	81 AA.
ID Q8K457			
AC Q8K457			
DT 01-OCT-2002 (TREMBlrel. 22, Created)			
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)			
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
DE Prokineticin 1 (Fragment).			
GN Name=Prok1; Synonyms=Pk1;			
OS Mus musculus (Mouse);			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_Taxid=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=C57BL/6;			
RX MEDLINE=2022134; PubMed=12024206; DOI=10.1038/417405a;			
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bernak J.C., Belluzzi J.,			
RA Weaver D.R., Leslie F.M., Zhou Q.Y.;			
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the			
RT suprachiasmatic nucleus.";			
RL Nature 417:405-410(2002).			
DR EMBL; AF487281; AAM49573.1; -.			
DR HSSP; P25687; 1IMT.			
DR MGD; MGI:2180370; Prok1.			
DR GO; GO:0005576; C:extracellular; IDA.			
DR GO; GO:0001877; P:activation of MAPK; IDA.			
DR GO; GO:0001623; P:circadian rhythm; TAS.			
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.			
DR GO; GO:0045765; P:regulation of angiogenesis; IDA.			
DR InterPro; IPR009523; Prokineticin.			
DR Pfam; PF06607; Prokineticin; 1.			
FT NON_TER			
SQ SEQUENCE	81 AA; 9192 MW; 7BBE3BC6B16A8011 CRC64;		
Query Match	86.7%; Score 432; DB 2; Length 81;		
Best local Similarity	87.7%; Pred. No. 3.5e-38;		
Matches	71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;		
QY	6 ACERDVQCGAGTCCAISLWLRGLRMCTPIGRGEGCHPSHKVPPFRKKKHTCPCLNVL 65		
Db	1 ACERDVQCGAGTCCAISLWLRGLRCLTPIGRGEGCHPSHKIPFLRKKOHHHTCPSPSL 60		
QY	66 LCSRFPDGRYRCSDMKKNF 86		
Db	61 LCSRFPDGRYRCSDMKKNF 81		
RESULT 2			
ID VPRA_DENPO			
AC P25687			
DT 01-MAY-1992 (Rel. 22, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Intestinal toxin 1 (MT1) (Venom protein A).
 OS Dendroaspis polylepsis polylepsis (Black mamba).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Elapidae; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Elapinae; Dendroaspis.
 NCBI_TaxID=8620;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=8115818; PubMed=7461607;
 RA Joubert F.J., Stridom D.J.;
 RT "Snake venom. The amino acid sequence of protein A from Dendroaspis
 polylepsis polylepsis (black mamba) venom."
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
 RA Schweitz H., Pascaud P., Diocot S., Moinier D., Lazdunski M.;
 RT "MT1, a black mamba toxin with a new and highly potent activity on
 intestinal contraction."
 RL Pfls Lett. 461:183-188(1998).
 RN [3]
 RP STRUCTURE BY NMR.
 RC TISSUE=Venom;
 RX MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
 RA Boibovier J., Albrand J.-P., Blackledge M., Jaquinod M.,
 RA Schweitz H., Lazdunski M., Marion D.;
 RT "A structural homologue of colipase in black mamba venom revealed by
 NMR floating disulphide bridge analysis."
 RL J. Mol. Biol. 283:205-219(1998).
 CC -1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the prokinectin family.
 DR PDB, 1MT; NMR, @1-81.
 DR InterPro: IPR009523; Prokinectin.
 DR Pfam: PF06607; Prokinectin; 1.
 KW 3D-structure; Direct protein sequencing; Toxin.
 FT DISULFID 7 19
 FT DISULFID 13 31
 FT DISULFID 18 60
 FT DISULFID 41 68
 FT DISULFID 62 78
 FT VARIANT 73 73
 FT VARIANT 18 18
 FT CONFLICT 22 22
 FT CONFLICT 18 18
 FT CONFLICT 22 22
 SQ SEQUENCE 81 AA; 8645 MW; 6C01368841572044 CRC64;
 P -> Q (in protein A').
 C -> S (in Ref. 1).
 S -> C (in Ref. 1).
 Query Match 62.3%; Score 310.5; DB 1; Length 81;
 Best local Similarity 62.8%; Pred. No. 2.4e-25;
 Matches 49; Conservative 14; Mismatches 14; Indels 1; Gaps 1;
 QY 1 AVITGACERDVOCAGTCCASISLMLRGLRMCTPLGRGESECHPSHNVPPFRKRK-HHTC 59
 DB 1 AVITGACERDVOCAGTCCASISLMLRGLRMCTPLGRGESECHPSHNVPPFRKRK-HHTC 60
 QY 60 PCLPNIILCSRFPPDGRYRC 77
 DB 61 PCAENLACVGTSPKFKKC 78
 RESULT 3
 TX16 PHORI STANDARD; PRT; 64 AA.
 ID TX16 PHORI
 AC P83893;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Non-toxic venom protein PRTX16CO.
 OS Phoneytria reidy (Brazilian Amazonian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneytria.
 NCBI_TaxID=272752;

RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
 RP SPECTROMETRY.
 RC TISSUE=Venom;
 RA Richardson M., Pimenta A.M.C., Benquerer M.P., Santoro M.M.,
 RA Figueiredo S.G., Cordelito M.N.;
 RT "Non-toxic protein PRTX16CO from venom of Brazilian Amazonian armed
 spider Phoneytria reidy has sequence similarities with toxins from
 other spiders."
 RL Submitted (APR-2004) to Swiss-Prot.
 CC -1- FUNCTION: Non-toxic to mice and insects.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- MASS SPECTROMETRY: MW=6981.39; METHOD=Electrospray; RANGE=1-64;
 CC NOTE=Ref.1.
 KW Direct protein sequencing.
 SQ SEQUENCE 64 AA; 6990 MW; 95E063A951261830 CRC64;
 Query Match 14.7%; Score 73; DB 1; Length 64;
 Best local Similarity 30.2%; Pred. No. 2.4;
 Matches 19; Conservative 5; Mismatches 29; Indels 10; Gaps 3;
 QY 7 CERDVOCAGTCCASISLMLRGLRMCTPLGRGESECH-PSHNVPPFRKRKHTCPCLPNT 65
 DB 3 CGSNADCGDCCCTGGSF--NRHCOSLADDTGTPCCKPNDYNEKX-----GCPKKEGL 53
 QY 66 LCS 68
 DB 54 ICS 56

RESULT 4
 TX16 PHONI STANDARD; PRT; 68 AA.
 ID TX16 PHONI
 AC P83997;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Non-toxic venom protein PNTX16CI.
 OS Phoneytria nigritventer (Brazilian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneytria.
 NCBI_TaxID=6918;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
 RP SPECTROMETRY, AND PYROLIDONE CARBOXYLIC ACID.
 RC TISSUE=Venom;
 RA Richardson M., Pimenta A.M.C., Benquerer M.P., Santoro M.M.,
 RA Figueiredo S.G., Cordelito M.N.;
 RT "Non-toxic protein PNTX16CI from venom of Brazilian armed spider
 Phoneytria nigritventer has sequence similarities with toxins from
 other spiders."
 RL Submitted (MAY-2004) to Swiss-Prot.
 CC -1- FUNCTION: Non-toxic to mice and insects.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- MASS SPECTROMETRY: MW=7666.6; METHOD=Electrospray; RANGE=1-68;
 CC NOTE=Ref.1.
 KW Direct protein sequencing; Pyroliidone carboxylic acid.
 FT MOD RBS 1 1
 FT MOD RBS 1 1
 SQ SEQUENCE 68 AA; 7605 MW; F7DF2844BFB5FCL CRC64;
 Query Match 14.1%; Score 70; DB 1; Length 68;
 Best local Similarity 27.5%; Pred. No. 5.3;
 Matches 19; Conservative 6; Mismatches 28; Indels 16; Gaps 3;
 QY 3 ITGACERDVOCAGTCCASISLMLRGLRMCTPLGRGESECHPSHNVPPFRKRKHT- 58
 DB 3 IPQSGCTNADCGDCCCTGGSY--NRHCOSLDDGKPCQ-----RPNKYDEYKFG 50
 QY 59 CPCLPNIILC 67
 DB 51 CPCKEGLMC 59

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RESULT 5
HEPC_MORCS
ID HEPC_MORCS STANDARD; PRT; 85 AA.
AC HEP2951;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hepcidin precursor.
OS Morone chrysops x Morone saxatilis (White bass x Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
NCBI_TaxId=45352;
(1)
SEQUENCE FROM N.A., SEQUENCE OF 65-85, TISSUE SPECIFICITY, ANTIBIOTIC
RP ACTIVITY, AND MASS SPECTROMETRY.
RC TISSUE-Gill, and Skin;
RX MEDLINE=21982021; PubMed=11985602;
RA Shire H., Lauth X., Western M.E., Ostland V.E., Carlberg J.M.,
RA Van Olet J.C., Shimizu C., Bulet P., Burns J.C.;
RT "Bass hepcidin is a novel antimicrobial peptide induced by bacterial
RT challenge."
RL Eur. J. Biochem. 269:2237-2237(2002).
CC -1- FUNCTION: Seems to act as a signaling molecule involved in the
CC maintenance of iron homeostasis. Seems to be regulated in
CC conjunction with HFE to regulate both intestinal iron absorption
CC and iron storage in macrophages (by similarity).
CC -1- FUNCTION: Antimicrobial activity against Gram-negative bacteria
CC such as E. coli.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in liver.
CC -1- INDUCTION: By bacterial challenge.
CC -1- MASS SPECTROMETRY: MW=2255.97; METHOD=MALDI; RANGE=65-85;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the hepcidin family.
-----
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-----
CC DR EMBL; AF394245; AAM28439.1; -.
CC DR EMBL; AF394246; AAM28440.1; -.
CC KW Antibiotic; Direct protein sequencing; Hormone; Signal.
CC FT SIGNAL 1 24 Potential.
CC FT PROPEP 25 64
CC FT PEPTIDE 65 85 Hepcidin.
CC FT DISULFID 66 72 Potential.
CC FT DISULFID 69 83 Potential.
CC FT DISULFID 70 82 Potential.
CC FT DISULFID 73 79 Potential.
CC SQ SEQUENCE 85 AA; 9484 MW; 0FEA55CF0A522C84 CRC64;
Query Match 13.3%; Score 66; DB 1; Length 85;
Best Local Similarity 30.0%; Pred. No. 18;
Matches 15; Conservative 8; Mismatches 15; Indels 12; Gaps 2;

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kappa-conotoxin Bx precursor.
OS Conus betulinus (Beech cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;
OC Neogastropoda; Conidae; Conidae; Conus.
NCBI_TaxId=89764;
(1)
SEQUENCE FROM N.A., SEQUENCE OF 27-43, AND MASS SPECTROMETRY.
RP TISSUE=Venom, and Venom duct;
RX PubMed=12547831; DOI=10.1074/jbc.M210200200;
RA Fan C.-X., Chen X.-K., Zhang C., Wang L.-X., Duan K.-L., He L.-L.,
RA Cao Y., Liu S.-Y., Zhong M.-N., Ulens C., Tytgat J., Chen J.-S.,
RA Chi C.-W., Zhou Z.;
RT "A novel conotoxin from Conus betulinus, kappa-Bx, unique in cysteine
RT pattern and in function as a specific BK channel modulator."
RL J. Biol. Chem. 278:12624-12633(2003).
CC -1- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
CC potassium channels. Modulator of potassium bind and inhibit voltage-sensitive
CC up-modulates the calcium and voltage-sensitive BK channels, has no
CC effect on single channel conductance, but increases the open
CC probability of BK channels.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- PTM: Contains four disulfide bonds.
CC -1- MASS SPECTROMETRY: MW=3569; METHOD=Electrospray; RANGE=27-57;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
CC family.
-----
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-----
CC DR EMBL; AF208661; AAF23167.1; -.
CC KW Amidation; Cleavage on pair of basic residues;
CC KW Direct protein sequencing; Gamma-carboxyglutamic acid; Hydroxylation;
CC KW Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
CC KW Signal; Toxin; Vitamin K.
CC FT SIGNAL 1 26
CC FT CHAIN 27 57 Kappa-conotoxin Bx.
CC FT PROPEP 61 70
CC FT MOD_RES 30 30 4-carboxyglutamate.
CC FT MOD_RES 35 35 4-carboxyglutamate.
CC FT MOD_RES 44 44 4-carboxyglutamate.
CC FT MOD_RES 53 53 Hydroxyproline.
CC FT MOD_RES 57 57 Proline amide (G-58 provides amide
CC group).
CC SQ SEQUENCE 70 AA; 7900 MW; F6575A2E30AD903 CRC64;
Query Match 12.8%; Score 63.5; DB 1; Length 70;
Best Local Similarity 37.3%; Pred. No. 27;
Matches 19; Conservative 1; Mismatches 14; Indels 17; Gaps 4;

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RESULT 6
CX2X_CONBE STANDARD; PRT; 70 AA.
ID CX2X_CONBE
AC Q9U3Z3;
DT 28-FEB-2003 (Rel. 41, Created)

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RESULT 7
Q9XXT6 PRELIMINARY; PRT; 83 AA.
ID Q9XXT6
AC Q9XXT6;
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Hypothetical protein Y1A5A.2.
GN ORFNames=Y1A5A.2;

```

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Briscot N2;
 RC MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Briscot N2;
 RA Barlow K.;
 RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021177; CAA15979.1; -.
 DR PIR; T26545; T26545.
 DR Wormbase; WBGene00012380; Y1A5A.2.
 DR WormPep; Y1A5A.2; CE20176.
 KW Hypothetical protein.
 SQ SEQUENCE 83 AA; 9318 MW; 9A9505953749C275 CRC64;
 QY Query Match 12.3%; Score 61.5; DB 2; Length 83;
 Best Local Similarity 37.5%; Pred. No. 51;
 Matches 18; Conservative 1; Mismatches 10; Indels 19; Gaps 3;
 Db 17 TCCTAATGATGCTPLGRGEGCHP-GSHKVPFFKRRKHTCTCP 63
 48 TCCCTISL-----GASAHPTSPRPV---RKQHTAPSP 77

RESULT 8

Q64DV8 PRELIMINARY; PRT; 50 AA.
 ID Q64DV8;
 AC Q64DV8;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=G217C7_38;
 OS uncultured archaean GZfos17C7.
 OC Archaea; environmental samples.
 OX NCBI_TaxID=285367;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=15353801;
 RA Hallam S.J.; Putnam N.; Preston C.M.; Dettler J.C.; Rokhsar D.;
 RA Richardson P.M.; Delong E.F.;
 RT "Reverse methanogenesis: testing the hypothesis with environmental
 RT genomes."
 RL Science 305:1457-1462(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Putnam N.; Dettler J.C.; Richardson P.M.; Rokhsar D.;
 RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY148822; AAU82419.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 50 AA; 6045 MW; 817208E41DD8986 CRC64;
 QY Query Match 11.7%; Score 58.5; DB 2; Length 50;
 Best Local Similarity 44.8%; Pred. No. 64;
 Matches 13; Conservative 1; Mismatches 14; Indels 1; Gaps 1;

RESULT 9
 Q64AE9 PRELIMINARY; PRT; 76 AA.

AC Q64AE9;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=G232E4_35;
 OS uncultured archaean GZfos32E4.
 OC Archaea; environmental samples.
 OX NCBI_TaxID=285379;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=15353801;
 RA Hallam S.J.; Putnam N.; Preston C.M.; Dettler J.C.; Rokhsar D.;
 RA Richardson P.M.; Delong E.F.;
 RT "Reverse methanogenesis: testing the hypothesis with environmental
 RT genomes."
 RL Science 305:1457-1462(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Putnam N.; Dettler J.C.; Richardson P.M.; Rokhsar D.;
 RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY14854; AAU83628.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 76 AA; 8760 MW; FE40SD4494703FB9 CRC64;
 QY Query Match 11.7%; Score 58.5; DB 1; Length 76;
 Best Local Similarity 44.8%; Pred. No. 97;
 Matches 13; Conservative 1; Mismatches 14; Indels 1; Gaps 1;
 Db 49 PFFKRRKHTCTCPCLPNLCSRPDPGRYRC 77
 39 PFFDKRQHRWA-CCPFSCPRFYQGHGIC 66

RESULT 10

ENAL_HORSE STANDARD; PRT; 46 AA.
 ID ENAL_HORSE
 AC P80930;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Antimicrobial peptide enAP-1 (Fragment).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Neutrophils;
 RX MEDLINE=92347972; PubMed=1639474;
 RA Cuto A.M.; Harwig S.S.L.; Cullor J.S.; Hughes J.P.; Lehrer R.I.;
 RT "Identification of enAP-1, an antimicrobial peptide from equine
 RT neutrophils."
 RL Infect. Immun. 60:3065-3071(1992).
 CC -1- FUNCTION: Has antimicrobial activity against Gram-negative and
 CC Gram-positive bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the granulin family.
 DR PIR; A44794; A44794.
 DR InterPro; IPR000118; Granulin.
 DR Pfam; PF00396; Granulin; 1.
 DR PROSITE; PS00799; GRANULINS; PARTIAL.
 KW Antimicrobial; Direct protein sequencing.
 FT DISULFID 4 16
 FT NON_TER 10 26
 FT 46 46
 SQ SEQUENCE 46 AA; 4888 MW; 2171934C15265862 CRC64;
 QY Query Match 11.6%; Score 58; DB 1; Length 46;
 Best Local Similarity 33.3%; Pred. No. 67;
 Matches 17; Conservative 3; Mismatches 23; Indels 8; Gaps 2;

QY 10 DVQAGATCAISLWRLGRLMCTPLGRGEGCHP-GSHKVPFFKRRKHTCTCP 60

Db 1 DVQCGSHFC-----HDXQTCRASGGXACCPGSGVCCADQR--HCCP 43

RESULT 11

ACTX_HADVE STANDARD; PRT; 68 AA.
 ID ACTX_HADVE STANDARD; PRT; 68 AA.
 AC P81803;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Atracotoxin-Hvfl7 (ActX-Hvfl7).
 OS Hadronyche versuta (Blue mountain funnel-web spider) (Atrax versuta).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mysgalomorphae; Hexathelidae; Hadronyche.
 OX NCBI_Taxid=6904;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Venom;
 RX MEDLINE=20132514; PubMed=10669030; DOI=10.1016/S0041-0101(99)00174-9;
 RA Szeto T.H., Wang X.-H., Smith R., Connor M., Christie M.J.,
 RA Nicholson G.M., King G.F.;
 RT Isolation of a funnel-web spider polypeptide with homology to mamba
 RT intestinal toxin 1 and the embryonic head inducer Dickkopf-1.";
 RL Toxicon 38:429-442(2000).
 CC -1- FUNCTION: Might aid in digestion of H. versuta prey. Not toxic to
 CC insects or mammals.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- PTM: Contains five disulfide bonds.
 KM Direct protein sequencing.
 SQ SEQUENCE 68 AA; 7564 MW; E9B6C345A6E5B8CF CRC64;

Query Match 11.5%; Score 57.5; DB 1; Length 68;
 Best Local Similarity 29.4%; Pred. No. 1.1e+02;
 Matches 20; Conservative 8; Mismatches 19; Indels 21; Gaps 5;

Qy 7 CERDVCGAGTCAISLWRLGRLMCTPLRGEGEC-----HPSGHVPEFKRHHC 59
 Db 3 CGDDV-CGASHCCSEYPPMH---CKRVGLYLCLAKSKATKNSGNHL--FF-----C 48

Qy 60 PCLPNDLC 67
 Db 49 PCDEGMVC 56

RESULT 12
 MT2_MUSAC STANDARD; PRT; 78 AA.

ID MT2_MUSAC STANDARD; PRT; 78 AA.
 AC 022319;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Metallochionein-like protein type 2.
 OS Musa acuminata (Banana).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
 OC Musa.
 OX NCBI_Taxid=4641;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Grand nain; TISSUE=Fruit flesh;
 RX MEDLINE=98002325; PubMed=9342866; DOI=10.1104/pp.115.2.463;
 RA Clendennen S.K., May G.D.;
 RT "Differential gene expression in ripening banana fruit.";
 RL Plant Physiol. 115:463-469(1997).
 CC -1- FUNCTION: Metallochioneins have a high content of cysteine
 CC residues that bind various heavy metals.
 CC -1- SIMILARITY: Belongs to the metallochionein superfamily. Family 15.
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CC -----
 CC EMBL; AF001525; AAB82774.1; ALT INIT.
 DR InterPro; IPR000347; Metallothion_15p.
 DR Pfam; PF01439; Metallothio_2; 1.
 DR ProDom; PD001611; Metallothion_15p; 1.
 KM Metal-binding; Metal-thiolate cluster.
 SQ SEQUENCE 78 AA; 7790 MW; 378B3EAEDEC217A98 CRC64;

Query Match 11.2%; Score 56; DB 1; Length 78;
 Best Local Similarity 44.0%; Pred. No. 1.8e+02;
 Matches 11; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

Qy 13 CGAGTCAISLWRLGRLMCTPLRGRE 37
 Db 8 CCGSSSCSCGSGCGGCRMLTDLGEE 32

RESULT 13

ID Q9PRN7 PRELIMINARY; PRT; 57 AA.
 AC Q9PRN7;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DE 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
 DE GGRN-GRANULIN-like peptide.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_Taxid=7957;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96051491; PubMed=8536941; DOI=10.1006/gen.1995.1113;
 RA Uesaka T., Yano K., Yamazaki M., Ando M.;
 RT "Somatostatin-, vasopressin-, and angiotensin-like
 RT peptides isolated from intestinal extracts of goldfish, Carassius
 RT auratus.";
 RL Gen. Comp. Endocrinol. 99:298-306(1995).
 DR HSSP; P81013; 118X.
 DR InterPro; IPR000118; Granulin.
 DR Pfam; PF00396; Granulin; 1.
 DR SMART; SM00277; GRAN; 1.
 SQ SEQUENCE 57 AA; 6321 MW; E4A12E4EC8901ABA CRC64;

Query Match 11.1%; Score 55.5; DB 2; Length 57;
 Best Local Similarity 32.5%; Pred. No. 1.5e+02;
 Matches 13; Conservative 5; Mismatches 19; Indels 3; Gaps 2;

Qy 7 CERDVCGAGTCAISLWRLGRLMCTPLRGEGECPPGSH 46
 Db 4 CDSSTICPDGTTCCISPY--GMYCCPFSM-GCCRDGHI 40

RESULT 14

ID Q7UUD0 PRELIMINARY; PRT; 76 AA.
 AC Q7UUD0;
 DT 01-OCT-2003 (TRENBLREL. 25, Created)
 DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
 DE Hypothetical protein.
 GN OrderededcussNames=RB3153;
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_Taxid=117;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
 RA Schlessner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planktonic ciliate *Pirellula* sp.
 strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294138; CAD73029.1; -;
 DR InterPro; IPR011477; DUF1584.
 DR Pfam; PF07623; PEGSRP; 1.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 76 AA; 8266 MW; B1349FB3B28D98B4 CRC64;

Query Match 11.1%; Score 55.5; DB 2; Length 76;
 Best Local Similarity 33.3%; Pred. No. 2e+02;
 Matches 13; Conservative 6; Mismatches 15; Indels 5; Gaps 1;

QY 33 PLGREGGECHPGS-----HVVFFRRKRKHTCCPLPNTL 66
 DB 8 PPGKEPERSHSATSLVHVVPKASQHRHSGPLVNVV 46

RESULT 15

Q96S92 PRELIMINARY; PRT; 80 AA.
 AC Q96S92;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li N., Zhang M., Wan T., Zhang W., Cao X.;
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY037153; AAK67633.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 80 AA; 9172 MW; 4745CB6B383AB10A CRC64;

Query Match 11.1%; Score 55.5; DB 2; Length 80;
 Best Local Similarity 29.4%; Pred. No. 2.1e+02;
 Matches 20; Conservative 6; Mismatches 29; Indels 13; Gaps 4;

QY 9 RDVOCAGTCCCAISIMLRLMCTPLFGRGEGCHGSHKVPFRRKRKHTCCPLPNTLCS 68
 DB 19 QSVFPGTSTYCV-----LNTVPPI--EDDHGNSNSGHVKIFLPKK--LLECLPK--CS 65
 QY 69 RPPDGRYR 76
 DB 66 SLPKERHR 73

Search completed: May 16, 2005, 06:52:34
 Job time : 177 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 06:35:01 ; Search time 161 Seconds
(without alignments)
206.593 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCGMKLNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1117955

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp19808:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20018:*\n5: geneseqp20028:*\n6: geneseqp20038:*\n7: geneseqp20038:*\n8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	4 AAB70146	Aab70146 Human G p
2	498	100.0	86	5 AAB76801	Abb76801 Human ZAQ
3	498	100.0	86	5 AAB705338	Abj05338 Human ZAQ
4	498	100.0	86	5 AAO15529	Aao15529 Human phy
5	498	100.0	86	5 ABB06306	Abb06306 Human G p
6	498	100.0	86	5 AAE24383	Aae24383 Human pro
7	498	100.0	86	7 ADD69104	Add69104 Human ZAQ
8	498	100.0	86	7 ADO05360	Ado05360 Human pro
9	498	100.0	86	8 ADN43256	Adn43256 Amino aci
10	498	100.0	86	8 ADR24003	Adr24003 Human ZAQ
11	497	99.8	86	4 AAB70145	Aab70145 Human G p
12	497	99.8	86	5 AAO15528	Aao15528 Human phy
13	497	99.8	86	5 ABB06305	Abb06305 Human G p
14	497	99.8	86	7 ADD69103	Add69103 Human ZAQ
15	497	99.8	86	8 ADR24004	Adr24004 Human ZAQ
16	494	99.2	85	5 AAE24393	Aae24393 Human pro
17	478	96.0	86	5 AAE24394	Aae24394 Human pro
18	473	95.0	86	5 ABB99154	Abb99154 Rat ZAQ p
19	473	95.0	86	5 ABB06959	Abb06959 Rat G pro
20	473	95.0	86	7 ADD69160	Add69160 Rat ZAQ-r
21	473	95.0	86	8 ADN43261	Adn43261 Amino aci
22	469	94.2	86	5 ABB99156	Abb99156 Rat ZAQ p
23	469	94.2	86	5 ABB06961	Abb06961 Rat G pro
24	469	94.2	86	7 ADD69164	Add69164 Rat ZAQ-r
25	467	93.8	86	5 ABB99155	Abb99155 Rat ZAQ p

26	467	93.8	86	5 ABB06960	Abb06960 Rat G pro
27	467	93.8	86	7 ADD69162	Add69162 Rat ZAQ-r
28	455	91.4	86	5 ABB99149	Abb99149 Mouse ZAQ
29	455	91.4	86	7 ADD69131	Add69131 Murine ZA
30	455	91.4	86	7 ADO05361	Ado05361 Mouse pro
31	455	91.4	86	8 ADN43259	Adn43259 Amino aci
32	413	82.9	86	5 AAE24391	Aae24391 Human pro
33	413	82.9	86	7 ADO05372	Ado05372 PK2/PK1 C
34	413	82.9	86	8 ADN43267	Adn43267 Amino aci
35	376	75.5	81	5 AAE24390	Aae24390 Human pro
36	376	75.5	81	7 ADO05371	Ado05371 PK1/PK2 C
37	376	75.5	81	8 ADN43266	Adn43266 Amino aci
38	361	72.5	81	2 AAY11745	Aay11745 Human 5'
39	357	71.7	80	3 AAG00617	Aag00617 Human sec
40	315	63.3	80	5 ABB99160	Abb99160 PolyIeipis
41	315	63.3	80	5 ABB99160	Abb99160 Dendroasp
42	315	63.3	80	5 ABB06310	Abb06310 Dendroasp
43	315	63.3	80	7 ADD69043	Add69043 Dendroasp
44	315	63.3	80	7 ADJ71812	Adj71812 Black mam
45	315	63.3	80	7 ADO05364	Ado05364 Snake pro

ALIGNMENTS

RESULT 1
AAB70146 standard; protein; 86 AA.
ID AAB70146
XX
AC AAB70146;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human G protein-coupled receptor protein-related sequence #2.
XX
KW Human; G protein-coupled receptor protein; neotropic; neuroprotective;
KW hypotensive; orexigenic; antiallergic; antidiabetic; antimicrobial;
KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
KW allergy; angina pectoris; infection; MRSA;
KW multiple resistant Staphylococcus aureus.
XX
OS Homo sapiens.
XX
PN WO200116309-A1.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP005685.
XX
PR 27-AUG-1999; 99JP-00241531.
PR 18-JUL-2000; 2000JP-00217474.
XX
PA (TAKEDA) TAKEDA CHEM IND LTD.
XX
PP Watanabe T, Terao Y, Shintani Y;
XX
DR WPI; 2001-226684/23.
XX
PT New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
PT hypertension and anorexia.
XX
PS Example 4; Fig 9; 119p; Japanese.
XX
CC The present sequence is provided in a specification relating to a protein
CC or its salt with an amino acid sequence identical or substantially
CC similar to a fully defined sequence of 393 amino acids as given in the
CC specification. The protein is useful in gene diagnosis and development of
CC preventives and remedies for diseases associated with dysfunction of the
CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
CC angina pectoris and infections (e.g. multiple resistant Staphylococcus
CC aureus). The proteins and DNA encoding the proteins are also useful for

CC the treatment of these diseases by gene therapy
XX
SQ Sequence 86 AA;

Query Match 100.0%; Score 498; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60
DB 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 2
ID ABB76801 standard; protein; 86 AA.
XX ABB76801;

XX 19-JUN-2002 (first entry)
XX Human ZAQ-1.

XX Recombinant protein production; drug; reagent; food stuff.
XX Homo sapiens.

XX WO200208417-A1.
XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-JP006392.
XX 25-JUL-2000; 2000JP-00229064.

XX (TAKE) TAKEDA CHEM IND LTD.
XX Ito T, Tanaka Y, Kondo M;

XX WPI; 2002-179906/23.
XX

PT Production of recombinant proteins in prokaryotes or eukaryotes
PT particularly with target proteins obtainable through gene recombination
PT technique, for use as drugs, reagents, raw materials for industries and
PT feeding stuffs.

PS Disclosure; Page 133; 137pp; Japanese.

CC The present invention relates to a method for producing recombinant
CC proteins. The method comprises preparing a recombinant vector for
CC transforming a host cell before culturing the obtained transformant,
CC assaying expression of the reporter gene and confirming high expression
CC of the reporter gene. The recombinant proteins are useful as drugs,
CC reagents, raw materials for industries and feeding stuffs. Also, the
CC proteins are obtainable on large-scale production. The present sequence
CC was used to illustrate the invention

XX Sequence 86 AA;

Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60
DB 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
XX

DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 3
ID ABB05338 standard; protein; 86 AA.
XX ABB05338;

XX 08-NOV-2002 (first entry)
XX Human ZAQ protein ligand.

XX Target peptide production; fusion peptide; protease-susceptible linker;
XX parathyroid hormone; PTH; high expression rate;
XX pharmaceutical application.

XX Homo sapiens.
XX WO200236762-A1.

XX 10-MAY-2002.
XX 29-OCT-2001; 2001WO-JP009476.

XX 30-OCT-2000; 2000JP-00331170.
XX 27-JUN-2001; 2001JP-00195522.

XX (TAKE) TAKEDA CHEM IND LTD.
XX Yamada T, Suenaga M;

XX WPI; 2002-417275/44.
XX DR N-PSDB; ABB06826.

PT Production of target peptide comprises cleavage of fusion peptide with
PT parathyroid hormone peptide for efficient manufacture of target peptide
PT without the need to remove N-terminal methionine.

XX Claim 14; Page 16; 103pp; Japanese.

CC The invention comprises a method of producing a target peptide. The C-
CC terminal end of the target peptide is fused via a protease-susceptible
CC linker to parathyroid hormone (PTH) residues 1-34. The method of the
CC invention is useful for the clean and efficient production of a target
CC peptide at a high expression rate on an industrial scale without the need
CC to remove the N-terminal methionine from the product. The peptides
CC produced by the method of the invention are suitable for pharmaceutical
CC and other uses. The present protein sequence was used in the invention

SQ Sequence 86 AA;

Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60
DB 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 4
ID AAO15529 standard; protein; 86 AA.
XX AAO15529;

XX 24-OCT-2002 (first entry)
XX

DE Human physiologically-active ZAQ ligand-related protein 4.
XX
KM Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
KW colitis; diarrhoea.
XX
OS Homo sapiens.
XX
PN WO200257443-A1.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-JP000378.
XX
PR 22-JAN-2001; 2001JP-00013027.
PR 17-MAY-2001; 2001JP-00147759.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Yamada T, Suenaga M, Nishimura O;
XX
DR WPI; 2002-566801/60.
XX
PT Industrial production of physiologically-active ZAQ ligand by expressing
PT in transformant prokaryote and refolding in redox buffer, for use in
PT preventing or treating digestive diseases e.g. colitis and diarrhoea.
XX
PS Claim 2; Page 79; 93pp; Japanese.
XX
CC The invention comprises a method for producing an active peptide that has
CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
CC method of the invention is useful for the production of a physiologically
CC -active ZAQ ligand for use in preventing or treating digestive diseases
CC (e.g. colitis and diarrhoea). The present amino acid sequence represents a
CC human physiologically active ZAQ ligand-related protein
XX
SQ Sequence 86 AA:
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLRGREGCHPGSHKVPFFRRKRNHTCP 60
DB 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLRGREGCHPGSHKVPFFRRKRNHTCP 60
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
RESULT 5
ABB06306
ID ABB06306 standard; protein; 86 AA.
XX
AC ABB06306;
XX
DT 27-MAY-2002 (first entry)
XX
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:21.
XX
KW G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
KW ZAQ; antidiarrhetic; laxative; drug development; digestive disease;
KW colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200206483-A1.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-JP006162.
XX
PR 18-JUL-2000; 2000JP-00217442.

PR 02-FEB-2001; 2001JP-00026779.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
XX
PI Hinuma S;
XX
DR WPI; 2002-188546/24.
DR N-PSDB; ABL49635.
XX
PT Physiologically-active peptides from cows milk, useful for developing
PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases
PT like colitis, diarrhoea, constipation and poor-absorption syndrome, by
PT gene therapy.
XX
PS Claim 1; Fig 9; 191pp; Japanese.
XX
CC The present invention describes a peptide containing an amino acid
CC sequence (I) identical to or substantially similar to that of the
CC sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrhetic and
CC laxative activities. The peptides and encoding DNAs from the present
CC invention are useful for developing drugs to treat digestive diseases
CC like colitis, diarrhoea, constipation and poor-absorption syndrome,
CC including gene therapy. The physiologically-active cows milk-originated
CC peptides are applicable as a specific ligand of brain-originated orphan G
CC protein-coupled receptor protein ZAQ. ABL49615 to ABB06059 and ABB06303
CC to ABB06315 represent sequences used in the exemplification of the
CC present invention
XX
SQ Sequence 86 AA:
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLRGREGCHPGSHKVPFFRRKRNHTCP 60
DB 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLRGREGCHPGSHKVPFFRRKRNHTCP 60
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
RESULT 6
AAE24383
ID AAE24383 standard; protein; 86 AA.
XX
AC AAE24383;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human prokineticin 1 mature protein.
XX
KW Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
KW diabetic gastroparesis; chronic constipation; malabsorptive disorder;
KW inflammatory bowel disorder; analgesic; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200236625-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US047969.
XX
PR 03-NOV-2000; 2000US-0245882P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zhou Q, Ehler FJ;
XX

DR WPI; 2002-479752/51.
DR N-PSDB; AAD39321.
XX
PT New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving impaired
PT gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation.
XX
PS Claim 1, Page 79-80, 86pp; English.
XX
CC The invention relates to human prokineticin 1 and 2 polypeptides that
CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
CC molecules encoding such polypeptides. Polypeptides of the invention are
CC useful for treating disorders involving impaired gastrointestinal
CC motility. They are useful for stimulating gastrointestinal motility in
CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
CC operational ileus, chronic constipation and gastrointestinal reflux
CC disease. The prokineticin antagonists are useful for inhibiting
CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
CC disorders, inflammatory bowel disorders, infectious diseases and
CC intestinal cancers. The antagonists also act as analgesics. The present
CC sequence is human prokineticin 1 mature protein
XX
SQ Sequence 86 AA;
XX
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AVITGACERDVQAGAGTCCASIMLRLGRLMCTPLGRGEGECHPSHKVPPFRKRKHHTCP 60
DB 1 AVITGACERDVQAGAGTCCASIMLRLGRLMCTPLGRGEGECHPSHKVPPFRKRKHHTCP 60
XX
QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
XX
RESULT 7
ADD69104
ID ADD69104 standard; protein; 86 AA.
XX
AC ADD69104;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human ZAO-related protein - SEQ ID 82.
XX
KW angiogenesis inhibitor; cytostatic; antiinflammatory; cancer;
KW ovarian disease; diabetic retinopathy; inflammatory; ZAO; Bv8; 15B;
KW human.
XX
OS Homo sapiens.
XX
PN WO2003066860-A1.
XX
PD 14-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-JP001057.
XX
PR 04-FEB-2002; 2002JP-00027299.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ohtaki T, Masuda Y, Takatsu Y;
XX
DR WPI; 2003-646310/61.
DR N-PSDB; ADD69110.
XX
PT Angiogenesis inhibitors for treatment and prevention of cancer, ovarian
PT diseases and inflammatory disease.
XX
PS Claim 1; SEQ ID NO 82; 308pp; Japanese.

XX
CC The invention relates to a novel angiogenesis inhibitor comprising a
CC compound that inhibits the activity of an amino acid sequence given in
CC the specification. Angiogenesis-related proteins Bv8, ZAO and 15B were
CC utilized within the method of the invention. The molecules of the
CC invention demonstrate cytostatic and antiinflammatory activities whilst
CC the method may be useful for treatment and prevention of cancer, ovarian
CC diseases, diabetic retinopathy and inflammatory disease. The current
CC sequence is that of the human ZAO-related protein of the invention.
XX
SQ Sequence 86 AA;
XX
Query Match 100.0%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AVITGACERDVQAGAGTCCASIMLRLGRLMCTPLGRGEGECHPSHKVPPFRKRKHHTCP 60
DB 1 AVITGACERDVQAGAGTCCASIMLRLGRLMCTPLGRGEGECHPSHKVPPFRKRKHHTCP 60
XX
QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
XX
RESULT 8
AD005360
ID AD005360 standard; protein; 86 AA.
XX
AC AD005360;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human prokineticin 1 (PK1), SEQ ID NO:9.
XX
KW Human; prokineticin 1; PK1; circadian rhythm; modulation; drug screening;
KW circadian rhythm disorder; non-24-hour sleep-wake syndrome;
KW rapid time-zone change syndrome; jetlag; work-shift syndrome;
KW delayed phase sleep syndrome; advanced sleep phase syndrome;
KW irregular sleep-wake pattern syndrome; decreased amplitude syndrome;
KW seasonal affective disorder; ultradian rhythm; daydreaming; urination;
KW hunger; infarctian rhythm; female sexual receptivity; CNS;
KW central nervous syndrome; PK2 receptor antagonist; PK2 receptor agonist.
XX
OS Homo sapiens.
XX
PN WO2003088904-A2.
XX
PD 30-OCT-2003.
XX
PF 15-APR-2003; 2003WO-US011538.
XX
PR 15-APR-2002; 2002US-0372836P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zhou Q, Bullock CM;
XX
DR WPI; 2003-854028/79.
XX
PT Screening for compounds for modulating circadian rhythm, for treating
PT seasonal disorders, comprises determining ability of prokineticin-2
PT receptor antagonist or agonist to modulate one or more circadian rhythm
PT function indicia.
XX
PS Disclosure; SEQ ID NO 9; 164pp; English.
XX
CC The invention relates to a method of screening for a compound for its
CC ability to modulate circadian rhythm. The method involved determining the
CC ability of a prokineticin 2 (PK2) receptor agonist or antagonist to
CC modulate one or more indicia or circadian rhythm function. The compound
CC is identified as being a PK2 receptor agonist or antagonist by
CC determining its effect on a predetermined signal such as calcium

XX
DR WPI; 2004-593431/57.
XX
PT New monoclonal antibody having high avidity to human ZAQ-1 polypeptide,
PT useful for preventing, treating or diagnosing diseases such as
PT endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS,
PT Parkinson's disease and diabetes.
XX
PS Claim 1; SEQ ID NO 1; 64pp; Japanese.
XX
CC The invention relates to a monoclonal antibody (I) having high avidity to
CC human ZAQ-1 ligand polypeptides, comprising either of two fully defined
CC sequences of 86 amino acids (S1). (I) is ZLI-107a or ZLI-234a produced
CC from hybridoma cells ZLI-107 FERM BP-8256 or ZLI-234 FERM BP-8257. (I) is
CC useful for carrying out assay of the polypeptide containing (S1) which
CC involves reacting (I) with the test-liquid containing the polypeptide or
CC its salt, and measuring the ratio of the polypeptide bound to (I). (I) is
CC useful as a diagnostic or therapeutic agent for diagnosis and/or
CC treatment of diseases such as endometrial cancer, endometriosis or
CC ovulation disorders, digestive diseases, diseases associated with
CC angiogenesis, diseases relating to pregnancy, eating disorder, sleeping
CC disorder, seasonal depression, reproductive dysfunction, endocrine
CC diseases, senile dementia, Alzheimer's disease, various disorders caused
CC by aging, cerebral circulatory disorder, head trauma, spinal injury,
CC epilepsy, anxiety, depression, manic depression, schizophrenia,
CC alcoholism, Parkinson's disease, hypertension, arteriosclerosis,
CC arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes,
CC etc. This sequence corresponds to a ZAQ-1 ligand used in the invention.
XX
SQ Sequence 86 AA;
XX
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGREGECHPSHKVPFRKRKHHTCP 60
1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGREGECHPSHKVPFRKRKHHTCP 60
XX
DB 61 CLPNLCSRPDDGRYRCMDLKNINF 86
61 CLPNLCSRPDDGRYRCMDLKNINF 86
XX
DB 61 CLPNLCSRPDDGRYRCMDLKNINF 86
61 CLPNLCSRPDDGRYRCMDLKNINF 86
XX
RESULT 11
AAB70145
ID AAB70145 standard; protein; 86 AA.
XX
AC AAB70145;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human G protein-coupled receptor protein-related sequence #1.
XX
KW Human; G protein-coupled receptor protein; natriuretic; neuroprotective;
KW hypotensive; orexigenic; anti-allergic; anti-inflam.; antimicrobial;
KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
KW allergy; angina pectoris; infection; MRSA;
KW multiple resistant Staphylococcus aureus.
XX
OS Homo sapiens.
XX
PN WO200116309-A1.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP005685.
XX
PR 27-AUG-1999; 99JP-00241531.
XX
PR 18-JUL-2000; 2000JP-00217474.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX

PI Watanabe T, Terao Y, Shintani Y;
XX
DR WPI; 2001-226684/23.
XX
PT New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
PT hypertension and anorexia.
XX
PS Example 4; Fig 9; 11pp; Japanese.
XX
CC The present sequence is provided in a specification relating to a protein
CC or its salt with an amino acid sequence identical or substantially
CC similar to a fully defined sequence of 393 amino acids as given in the
CC specification. The protein is useful in gene diagnosis and development of
CC preventives and remedies for diseases associated with dysfunction of the
CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
CC angina pectoris and infections (e.g. multiple resistant Staphylococcus
CC aureus. The proteins and DNA encoding the proteins are also useful for
CC the treatment of these diseases by gene therapy
XX
SQ Sequence 86 AA;
XX
Query Match 99.8%; Score 497; DB 4; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGREGECHPSHKVPFRKRKHHTCP 60
1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGREGECHPSHKVPFRKRKHHTCP 60
XX
DB 61 CLPNLCSRPDDGRYRCMDLKNINF 86
61 CLPNLCSRPDDGRYRCMDLKNINF 86
XX
DB 61 CLPNLCSRPDDGRYRCMDLKNINF 86
61 CLPNLCSRPDDGRYRCMDLKNINF 86
XX
RESULT 12
AA015528
ID AA015528 standard; protein; 86 AA.
XX
AC AA015528;
XX
DT 24-OCT-2002 (first entry)
XX
DE Human physiologically-active ZAQ ligand-related protein 3.
XX
KW Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
KW colitis; diarrhoea.
XX
OS Homo sapiens.
XX
PN WO200257443-A1.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-JP000378.
XX
PR 22-JAN-2001; 2001JP-00013027.
XX
PR 17-MAY-2001; 2001JP-00147759.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Yamada T, Suenaga M, Nishimura O;
XX
DR WPI; 2002-566801/60.
XX
PT Industrial production of physiologically-active ZAQ ligand by expressing
PT in transformant prokaryote and refolding in redox buffer, for use in
PT preventing or treating digestive diseases e.g. colitis and diarrhea.
XX
PS Claim 4; Page 78; 93pp; Japanese.
XX
CC The invention comprises a method for producing an active peptide that has

CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
CC method of the invention is useful for the production of a physiologically
CC active ZAQ ligand for use in preventing or treating digestive diseases
CC (e.g. colitis and diarrhea). The present amino acid sequence represents a
CC human physiologically active ZAQ ligand-related protein
XX

Sequence 86 AA:

Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKVPFRKRKHTCP 60
DB 1 AVITGACERDVOCAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKVPFRKRKHTCP 60

QY 61 CLPNLCSRPDPGRYRCMDLNINF 86
DB 61 CLPNLCSRPDPGRYRCMDLNINF 86

RESULT 13

ABB06305 standard; protein; 86 AA.

ABB06305;

27-MAY-2002 (first entry)

Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:20.

G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;
KW colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.

Homo sapiens.

WO200206483-A1.

24-JAN-2002.

17-JUL-2001; 2001WO-JP006162.

18-JUL-2000; 2000JP-00217442.

02-FEB-2001; 2001JP-00026779.

(TAKE) TAKEDA CHEM IND LTD.

Ohtaki T, Maesuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;

Hinuma S;

WPI; 2002-188546/24.

N-PSDB; ABL49634.

Physiologically-active peptides from cows milk, useful for developing
PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases
PT like colitis, diarrhea, constipation and poor-absorption syndrome, by
PT gene therapy.

Claim 1; Fig 9; 191pp; Japanese.

The present invention describes a peptide containing an amino acid.

Sequence (1) identical to or substantially similar to that of the

sequences in ABB06305 or ABB06306, or its salt. (1) has antidiarrheic and

laxative activities. The peptides and encoding DNAs from the present

invention are useful for developing drugs to treat digestive diseases

like colitis, diarrhoea, constipation and poor-absorption syndrome,
including gene therapy. The physiologically-active cows milk-originated
peptides are applicable as a specific ligand of brain-originated orphan G
protein-coupled receptor protein ZAQ. ABL49615 to ABB40659 and ABB06303
to ABB06315 represent sequences used in the exemplification of the
present invention

Sequence 86 AA:

Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKVPFRKRKHTCP 60
DB 1 AVITGACERDVOCAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKVPFRKRKHTCP 60

QY 61 CLPNLCSRPDPGRYRCMDLNINF 86
DB 61 CLPNLCSRPDPGRYRCMDLNINF 86

RESULT 14

ADD69103 standard; protein; 86 AA.

ADD69103;

15-JAN-2004 (first entry)

Human ZAQ-related protein - SEQ ID 81.

angiogenesis inhibitor; cyrostatic; antiinflammatory; cancer;
KW ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; 15E;
KW human.

Homo sapiens.

WO2003066860-A1.

14-AUG-2003.

03-FEB-2003; 2003WO-JP001057.

04-FEB-2002; 2002JP-00027299.

(TAKE) TAKEDA CHEM IND LTD.

Ohtaki T, Maesuda Y, Takatsu Y;

WPI; 2003-646310/61.

N-PSDB; ADD69109.

Angiogenesis inhibitors for treatment and prevention of cancer, ovarian
PT diseases and inflammatory disease.

Claim 1; SEQ ID NO 81; 308pp; Japanese.

The invention relates to a novel angiogenesis inhibitor comprising a

compound that inhibits the activity of an amino acid sequence given in

the specification. Angiogenesis-related proteins Bv8, ZAQ and 15E were

utilised within the method of the invention. The molecules of the

invention demonstrate cyrostatic and antiinflammatory activities whilst

the method may be useful for treatment and prevention of cancer, ovarian

diseases, diabetic retinopathy and inflammatory disease. The current

sequence is that of the human ZAQ-related protein of the invention.

Sequence 86 AA:

Query Match 99.8%; Score 497; DB 7; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKVPFRKRKHTCP 60
DB 1 AVITGACERDVOCAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKVPFRKRKHTCP 60

QY 61 CLPNLCSRPDPGRYRCMDLNINF 86
DB 61 CLPNLCSRPDPGRYRCMDLNINF 86

RESULT 15

ADNR24004

ID ADNR24004 standard; protein; 86 AA.

XX ADNR24004;

DT 21-OCT-2004 (first entry)

XX Human ZAO-1 ligand protein #2.

XX antiangiogenic; antialcoholic; antiarrhythmic; antiarteriosclerotic;
 KW anticonvulsant; antidepressant; antidiabetic; anti-HIV; antineoplastic;
 KW antiparkinsonian; cerebroprotective; cytoskeletal; eating disorders;
 KW endocrine; gastroenteric; gynecological; hypnotic; hypotensive;
 KW neuroleptic; neuroprotective; nootropic; ophthalmological; tranquilizer;
 KW vasotropic; vulnery; monoclonal antibody; human; ZAO-1; ligand;
 KW hybridoma cell; assay; diagnosis; endometrial cancer; endometriosis;
 KW ovulation disorder; digestive disease; angiogenesis; pregnancy;
 KW eating disorder; sleeping disorder; seasonal depression;
 KW reproductive dysfunction; endocrine disease; senile dementia;
 KW Alzheimer's disease; aging; cerebral circulatory disorder; head trauma;
 KW spinal injury; epilepsy; anxiety; depression; schizophrenia; alcoholism;
 KW Parkinson's disease; hypertension; arteriosclerosis; arrhythmia;
 KW premenstrual disorder syndrome; glaucoma; AIDS; diabetes.

XX Homo sapiens.

OS WO2004065419-A1.

XX 05-AUG-2004.

XX 21-JAN-2004; 2004WO-JP000498.

XX 22-JAN-2003; 2003JP-00014055.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Matsumoto H, Horikoshi Y, Masuda Y, Ohtaki T;

XX WPI; 2004-593431/57.

XX New monoclonal antibody having high avidity to human ZAO-1 polypeptide,
 PT useful for preventing, treating or diagnosing diseases such as
 PT endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS,
 PT Parkinson's disease and diabetes.

PS Claim 1; SEQ ID NO 2; 64pp; Japanese.

XX The invention relates to a monoclonal antibody (I) having high avidity to
 CC human ZAO-1 ligand polypeptides, comprising either of two fully defined
 CC sequences of 86 amino acids (S1). (I) is ZL1-107a or ZL1-234a produced
 CC from hybridoma cells ZL1-107 FERM BP-8256 or ZL1-234 FERM BP-8257. (I) is
 CC useful for carrying out assay of the polypeptide containing (S1) which
 CC involves reacting (I) with the test-liquid containing the polypeptide or
 CC its salt, and measuring the ratio of the polypeptide bound to (I). (I) is
 CC useful as a diagnostic or therapeutic agent for diagnosis and/or
 CC treatment of diseases such as endometrial cancer, endometriosis or
 CC ovulation disorders, digestive diseases, diseases associated with
 CC angiogenesis, diseases relating to pregnancy, eating disorder, sleeping
 CC disorder, seasonal depression, reproductive dysfunction, endocrine
 CC diseases, senile dementia, Alzheimer's disease, various disorders caused
 CC by aging, cerebral circulatory disorder, head trauma, spinal injury,
 CC epilepsy, anxiety, depression, manic depression, schizophrenia,
 CC alcoholism, Parkinson's disease, hypertension, arteriosclerosis,
 CC arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes,
 CC etc. This sequence corresponds to a ZAO-1 ligand used in the invention.

XX Sequence 86 AA;

Query Match 99.8%; Score 497; DB 8; Length 86;
 Best Local Similarity 98.8%; Pred. No. 9.5e-47;

	Matches	85; Conservative	1; Mismatches	0; Indels	0; Gaps	0;
QY	1	AVITGACERDVCGAGTCCATSLMRLRMCTPLGRGEBCHPGSHKVPFRKRKHHTCP	60			
Db	1	AVITGACERDVCGAGTCCATSLMRLRMCTPLGRGEBCHPGSHKVPFRKRKHHTCP	60			
QY	61	CLPNLLCSRFPDGRYRCSDMLKNINF	86			
Db	61	CLPNLLCSRFPDGRYRCSDMLKNINF	86			

Search completed: May 16, 2005, 06:49:32
 Job time : 162 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 06:52:43 / Search time 132 Seconds
(without alignments)
217.640 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498
Sequence: 1 AVITGACERDVCGAGTCCA.....CSRFPGRYRCMDLNINF 86

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 575500

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US61_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US61_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US61_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	86	13	US-10-016-481-3
2	498	100.0	86	14	US-10-323-157-3
3	498	100.0	86	15	US-10-417-426-9
4	498	100.0	86	15	US-10-333-192-21
5	498	100.0	86	17	US-10-811-328-3
6	498	100.0	86	17	US-10-912-907-3
7	498	100.0	86	17	US-10-415-724-3
8	497	99.8	86	15	US-10-333-192-20
9	494	99.2	85	13	US-10-016-481-16
10	494	99.2	85	14	US-10-323-157-16
11	494	99.2	85	17	US-10-811-328-16
12	494	99.2	85	17	US-10-912-907-16
13	494	99.2	85	17	US-10-415-724-16

14	494	99.2	86	17	US-10-811-328-20	Sequence 20, Appl
15	478	96.0	86	13	US-10-016-481-17	Sequence 17, Appl
16	478	96.0	86	14	US-10-323-157-17	Sequence 17, Appl
17	478	96.0	86	17	US-10-811-328-17	Sequence 17, Appl
18	478	96.0	86	17	US-10-912-907-17	Sequence 17, Appl
19	478	96.0	86	17	US-10-415-724-17	Sequence 17, Appl
20	473	95.0	86	15	US-10-470-951-37	Sequence 37, Appl
21	473	95.0	86	15	US-10-362-504-49	Sequence 49, Appl
22	473	95.0	86	17	US-10-811-328-10	Sequence 30, Appl
23	469	94.2	86	15	US-10-470-951-8	Sequence 41, Appl
24	469	94.2	86	15	US-10-362-504-53	Sequence 53, Appl
25	467	93.8	86	15	US-10-470-951-51	Sequence 39, Appl
26	467	93.8	86	16	US-10-362-504-51	Sequence 51, Appl
27	455	91.4	86	15	US-10-417-426-10	Sequence 10, Appl
28	455	91.4	86	15	US-10-470-951-8	Sequence 8, Appl
29	455	91.4	86	17	US-10-811-328-28	Sequence 28, Appl
30	413	82.9	86	13	US-10-016-481-14	Sequence 14, Appl
31	413	82.9	86	14	US-10-323-157-14	Sequence 14, Appl
32	413	82.9	86	15	US-10-417-426-21	Sequence 21, Appl
33	413	82.9	86	17	US-10-811-328-14	Sequence 14, Appl
34	413	82.9	86	17	US-10-912-907-14	Sequence 14, Appl
35	413	82.9	86	17	US-10-415-724-14	Sequence 14, Appl
36	376	75.5	81	13	US-10-016-481-13	Sequence 13, Appl
37	376	75.5	81	14	US-10-323-157-13	Sequence 13, Appl
38	376	75.5	81	15	US-10-417-426-20	Sequence 20, Appl
39	376	75.5	81	17	US-10-811-328-13	Sequence 13, Appl
40	376	75.5	81	17	US-10-912-907-13	Sequence 13, Appl
41	376	75.5	81	17	US-10-415-724-13	Sequence 13, Appl
42	315	63.3	80	15	US-10-417-426-13	Sequence 13, Appl
43	315	63.3	80	15	US-10-467-019-21	Sequence 21, Appl
44	315	63.3	80	15	US-10-470-951-64	Sequence 64, Appl
45	315	63.3	80	15	US-10-333-192-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-10-016-481-3
; Sequence 3, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-481-3

Query Match 100.0%; Score 498; DB 13; length 86;
Best local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCAISLMRGLMCTPLRGEGECPGSHKVPFRKRKHHTP 60
|||
DB 1 AVITGACERDVCGAGTCCAISLMRGLMCTPLRGEGECPGSHKVPFRKRKHHTP 60

QY 61 CLPNILCSRFPGRYRCMDLNINF 86
|||
DB 61 CLPNILCSRFPGRYRCMDLNINF 86

RESULT 2

US-10-323-157-3
; Sequence 3, Application US/10323157
; Publication No. US20030113867A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-323-157-3

Query Match 100.0%; Score 498; DB 14; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
QY 61 CLPNLLCSRPPDGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRPPDGRYRCSDMLKNINF 86

RESULT 3
US-10-417-426-9
; Sequence 9, Application US/10417426
; Publication No. US20030235535A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Bullock, Clayton M.
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Treating Circadian Rhythm Disorders
; FILE REFERENCE: P-UC 5773
; CURRENT APPLICATION NUMBER: US/10/417,426
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/372,836
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-426-9

Query Match 100.0%; Score 498; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
QY 61 CLPNLLCSRPPDGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRPPDGRYRCSDMLKNINF 86

RESULT 4
US-10-333-192-21

; Sequence 21, Application US/10333192
; Publication No. US20040077535A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: MATANABE, Takuya
; APPLICANT: TERAO, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/10/333,192
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human
US-10-333-192-21

Query Match 100.0%; Score 498; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
QY 61 CLPNLLCSRPPDGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRPPDGRYRCSDMLKNINF 86

RESULT 5
US-10-811-328-3
; Sequence 3, Application US/10811328
; Publication No. US20050026828A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-811-328-3

Query Match 100.0%; Score 498; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
QY 61 CLPNLLCSRPPDGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRPPDGRYRCSDMLKNINF 86

RESULT 6

US-10-912-907-3
; Sequence 3, Application US/10912907
; Publication No. US20050037464A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokinection Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/912,907
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-912-907-3

Query Match
Best Local Similarity 100.0%; Score 498; DB 17; Length 86;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCCAISIMLRGLMCTPLGRGEGCHGSHKVPFFRKXKHTCP 60
DB 1 AVITGACERDVCGAGTCCCAISIMLRGLMCTPLGRGEGCHGSHKVPFFRKXKHTCP 60

QY 61 CLPNLCRFPDGRYRCSDMLKKNIF 86
DB 61 CLPNLCRFPDGRYRCSDMLKKNIF 86

RESULT 7

US-10-415-724-3
; Sequence 3, Application US/10415724
; Publication No. US20050074758A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Prokinection Polypeptides, Related
; FILE REFERENCE: PP-UC 5030
; CURRENT APPLICATION NUMBER: US/10/415,724
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-724-3

Query Match
Best Local Similarity 100.0%; Score 498; DB 17; Length 86;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCCAISIMLRGLMCTPLGRGEGCHGSHKVPFFRKXKHTCP 60
DB 1 AVITGACERDVCGAGTCCCAISIMLRGLMCTPLGRGEGCHGSHKVPFFRKXKHTCP 60

QY 61 CLPNLCRFPDGRYRCSDMLKKNIF 86
DB 61 CLPNLCRFPDGRYRCSDMLKKNIF 86

RESULT 8

US-10-333-192-20

; Sequence 20, Application US/10333192
; Publication No. US20040077535A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAU, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/10/333,192
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 20
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human
US-10-333-192-20

Query Match
Best Local Similarity 99.8%; Score 497; DB 15; Length 86;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCCAISIMLRGLMCTPLGRGEGCHGSHKVPFFRKXKHTCP 60
DB 1 AVITGACERDVCGAGTCCCAISIMLRGLMCTPLGRGEGCHGSHKVPFFRKXKHTCP 60

QY 61 CLPNLCRFPDGRYRCSDMLKKNIF 86
DB 61 CLPNLCRFPDGRYRCSDMLKKNIF 86

RESULT 9

US-10-016-481-16
; Sequence 16, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokinection Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic construct
US-10-016-481-16

Query Match
Best Local Similarity 99.2%; Score 494; DB 13; Length 85;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VITGACERDVCGAGTCCCAISIMLRGLMCTPLGRGEGCHGSHKVPFFRKXKHTCP 61
DB 1 VITGACERDVCGAGTCCCAISIMLRGLMCTPLGRGEGCHGSHKVPFFRKXKHTCP 60

QY 62 LPNLLCSRFPDGRYRCMDLKNINF 86
 |||||
Db 61 LPNLLCSRFPDGRYRCMDLKNINF 85

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RESULT 10
US-10-323-157-16
; Sequence 16, Application US/10323157
; Publication No. US20030113867A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehlet, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-323-157-16

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Qy	2	VITGACRDVDCGAGTCCCAISLMTLRLGRLMCTPLGREGEGCHSGSHKVFPRKRKHHTGRC	61
Db	1	VITACGRDVGCGAGTCCCAISLMTLRLGRLMCTPLGREGEGCHSGSHKVFPRKRKHHTGRC	60
Qy	62	LPNLLCRFPDGRRCRCSMDLNNINF	86
Db	61	LPNLLCRFPDGRRCRCSMDLNNINF	85

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RESULT 11
US-10-811-328-16
; Sequence 16, Application US/10811328
; Publication No.: US20050026828A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion:
; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ. ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-10-811-328-16

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Query Match      99.2%  Score 494;  DB 17;  Length 85;
Best Local Similarity 100.0%;  Pred. No. 5.2e-45;
Matches      85;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

      2  VTGACRDVQCGAGTCCATSLWLRGMCTPLRGEGBEGCHSGHKVDFPKRRKHHNCPG  61
      |||||||

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Db 1 VTGAGERDYQGCAGTCAISLIRLRNCTPLRGEGEGSHKVPFRKRKHTTC 60

Qy 62 LPYLCSRFPDGYRCSMDLKNINF 86
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61 LPYLCSRFPDGYRCSMDLKNINF 85

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RESULT 12
US-10-912-907-16
; Sequence 16, Application US/10912507
; Publication No. US2005003774641
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokination Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/912,907
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-10-912-907-16

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	Query Match	Best Local Similarity	99.2%;	Score 494;	DB 17/;	Length 85;
	Matches	Conservative	0;	Pred. No. 5,2e-45;	Mismatches 0;	Indels 0; Gaps 0;
Qy	2	VINGACRDVDCGAGTCCATSLIMLRGIRMCPTLGRGEGEGCHPSGHKVPFRKRKHHTPC	61			
Db	1	VINGACERDVDCGAGTCCATSLIMLRGIRMCPTLGRGEGEGCHPSGHKVPFRKRKHHTPC	60			
Qy	62	LPNLLCSRPDPGRYRCMDLKNINF	86			
Db	61	LPNLLCSRPDPGRYRCMDLKNINF	85			

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RESULT 13
US-10-415-724-16
; Sequence 16, Application US/10415724
; Publication No. US20050074758A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Prokinestin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: PP-UC 5030
; CURRENT APPLICATION NUMBER: US/10/415,724
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/745,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-10-415-724-16

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Query Match	99.2%	Score 494	DB 17	Length 85
Best Local Similarity	100.0%	Pred. No. 5.2e-45		
Matches 85; Conservative	0	Mismatches 0	Indels 0	Gaps 0

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OM protein - protein search, using sw model

Run on: May 16, 2005, 06:46:53 ; Search time 481 Seconds
(without alignments)
208.833 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498
Sequence: 1 AVITGACERDVGAGAGTCCA.....CSNFRGGRYRCMDLKNIF 86

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 3944151

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main:*

1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
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4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
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33: /cgn2_6/ptodata/1/paa/US107_COMB.pep.*
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37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	1	PCT-US00-05226-35
2	498	100.0	86	1	PCT-US03-11538-9
3	498	100.0	86	1	PCT-US03-31626-5
4	498	100.0	86	1	PCT-US04-09255-3
5	498	100.0	86	19	US-09-516-745-35
6	498	100.0	86	26	US-10-016-481-3
7	498	100.0	86	26	US-10-016-481A-3
8	498	100.0	86	26	US-10-070-240A-21
9	498	100.0	86	26	US-10-070-240A-34
10	498	100.0	86	29	US-10-323-157-3
11	498	100.0	86	29	US-10-323-157A-3
12	498	100.0	86	29	US-10-333-152-21
13	498	100.0	86	29	US-10-343-095A-117
14	498	100.0	86	30	US-10-415-724A-3
15	498	100.0	86	30	US-10-415-724A-3
16	498	100.0	86	30	US-10-417-426-9
17	498	100.0	86	32	US-10-680-554-5
18	498	100.0	86	33	US-10-713-567-3
19	498	100.0	86	34	US-10-811-328-3
20	498	100.0	86	35	US-10-912-907-3
21	498	100.0	86	37	US-60-426-203-3
22	498	100.0	86	37	US-60-457-891-3
23	497	99.8	86	26	US-10-070-240A-20
24	497	99.8	86	26	US-10-070-240A-33
25	497	99.8	86	29	US-10-333-192-20
26	494	99.2	85	1	PCT-US04-09255-16
27	494	99.2	85	26	US-10-016-481A-16
28	494	99.2	85	26	US-10-016-481A-16
29	494	99.2	85	29	US-10-323-157-16
30	494	99.2	85	29	US-10-323-157A-16
31	494	99.2	85	30	US-10-415-724A-16
32	494	99.2	85	30	US-10-415-724A-16
33	494	99.2	85	33	US-10-713-567-16
34	494	99.2	85	34	US-10-811-328-16
35	494	99.2	85	35	US-10-912-907-16
36	494	99.2	85	37	US-60-426-203-16
37	494	99.2	85	37	US-60-457-891-16
38	494	99.2	86	1	PCT-US04-09255-20
39	494	99.2	86	33	US-10-713-567-20
40	494	99.2	86	34	US-10-811-328-20
41	494	99.2	86	37	US-60-426-203-20
42	494	99.2	86	37	US-60-457-891-20
43	494	99.2	86	1	PCT-US04-09255-17
44	478	96.0	86	26	US-10-016-481-17
45	478	96.0	86	26	US-10-016-481A-17

ALIGNMENTS

RESULT 1
PCT-US00-05226-35
; Sequence 35, Application PC/TUS0005226
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THEM
; FILE REFERENCE: 7853-191-228
; CURRENT APPLICATION NUMBER: PCT/US00/05226
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-05226-35

Db 1 AVITACERDVOCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFFRKRGHTCP 60

Qy 61 CLPNLCSRFPDGRYRCSDMLKNINF 86

Db 61 CLPNLCSRFPDGRYRCSDMLKNINF 86

RESULT 6

US-10-016-481-3
; Sequence 3, Application US/10016481
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokinection Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-481-3

Query Match 100.0%; Score 498; DB 26; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AVITACERDVOCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFFRKRGHTCP 60

Qy 61 CLPNLCSRFPDGRYRCSDMLKNINF 86

Db 61 CLPNLCSRFPDGRYRCSDMLKNINF 86

RESULT 7

US-10-016-481A-3
; Sequence 3, Application US/10016481A
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokinection Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481A
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-481A-3

Query Match 100.0%; Score 498; DB 26; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITACERDVOCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFFRKRGHTCP 60

Db 1 AVITACERDVOCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFFRKRGHTCP 60

Qy 61 CLPNLCSRFPDGRYRCSDMLKNINF 86

Db 61 CLPNLCSRFPDGRYRCSDMLKNINF 86

RESULT 8

US-10-070-240A-21
; Sequence 21, Application US/10070240A
; GENERAL INFORMATION:
; APPLICANT: WATANABE, TAKUYA
; APPLICANT: TERAU, YASUOKO
; APPLICANT: SHINTANI, YASUSHI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN AND DNA
; FILE REFERENCE: (46342) 57127
; CURRENT APPLICATION NUMBER: US/10/070,240A
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: JP 2000-217474
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JO 11-241531
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: PCT/JP00/05685
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-070-240A-21

Query Match 100.0%; Score 498; DB 26; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITACERDVOCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFFRKRGHTCP 60

Db 1 AVITACERDVOCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFFRKRGHTCP 60

Qy 61 CLPNLCSRFPDGRYRCSDMLKNINF 86

Db 61 CLPNLCSRFPDGRYRCSDMLKNINF 86

RESULT 9

US-10-070-240A-34
; Sequence 34, Application US/10070240A
; GENERAL INFORMATION:
; APPLICANT: WATANABE, TAKUYA
; APPLICANT: TERAU, YASUOKO
; APPLICANT: SHINTANI, YASUSHI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN AND DNA
; FILE REFERENCE: (46342) 57127
; CURRENT APPLICATION NUMBER: US/10/070,240A
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: JP 2000-217474
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JO 11-241531
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: PCT/JP00/05685
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-070-240A-34

Query Match 100.0%; Score 498; DB 26; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AVITGACERDVOCGAGTCCCAISIMLRGLRMCTPLGRBEGECHPGSHKVPFFRKXKHTCP 60
QY 61 CLPNILCSRFPDGRYRCMDLKNINF 86
Db 61 CLPNILCSRFPDGRYRCMDLKNINF 86

RESULT 10
US-10-323-157-3
; Sequence 3, Application US/10323157
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-323-157-3

Query Match 100.0%; Score 498; DB 29; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVOCGAGTCCCAISIMLRGLRMCTPLGRBEGECHPGSHKVPFFRKXKHTCP 60
Db 1 AVITGACERDVOCGAGTCCCAISIMLRGLRMCTPLGRBEGECHPGSHKVPFFRKXKHTCP 60
QY 61 CLPNILCSRFPDGRYRCMDLKNINF 86
Db 61 CLPNILCSRFPDGRYRCMDLKNINF 86

RESULT 11
US-10-323-157A-3
; Sequence 3, Application US/10323157A
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: 66678-144 (UC 5534)
; CURRENT APPLICATION NUMBER: US/10/323,157A
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 10/016,481
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-323-157A-3

Query Match 100.0%; Score 498; DB 29; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVOCGAGTCCCAISIMLRGLRMCTPLGRBEGECHPGSHKVPFFRKXKHTCP 60
Db 1 AVITGACERDVOCGAGTCCCAISIMLRGLRMCTPLGRBEGECHPGSHKVPFFRKXKHTCP 60

QY 61 CLPNILCSRFPDGRYRCMDLKNINF 86
Db 61 CLPNILCSRFPDGRYRCMDLKNINF 86

RESULT 12
US-10-333-192-21
; Sequence 21, Application US/10333192
; GENERAL INFORMATION:
; APPLICANT: OHTANI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAO, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HIMUDA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human
US-10-333-192-21

Query Match 100.0%; Score 498; DB 29; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AVITGACERDVOCGAGTCCCAISIMLRGLRMCTPLGRBEGECHPGSHKVPFFRKXKHTCP 60
QY 61 CLPNILCSRFPDGRYRCMDLKNINF 86
Db 61 CLPNILCSRFPDGRYRCMDLKNINF 86

RESULT 13
US-10-343-095A-117
; Sequence 117, Application US/10343095A
; GENERAL INFORMATION:
; APPLICANT: ITO, Takashi
; APPLICANT: TANAKA, Yoko
; APPLICANT: KONDO, Mitsuyo
; TITLE OF INVENTION: Process for Producing Recombinant Protein
; FILE REFERENCE: 2764USOP
; CURRENT APPLICATION NUMBER: US/10/343,095A
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/JP01/06392
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: JP 2000-229064
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 122
; SEQ ID NO 117
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human
US-10-343-095A-117

Query Match 100.0%; Score 498; DB 29; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCGAGTCCCAISLMLRGLMCTPLGRGEGECHGSHKVPFFRRKRNHTCP 60
DB 1 AVITGACERDVOCGAGTCCCAISLMLRGLMCTPLGRGEGECHGSHKVPFFRRKRNHTCP 60
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86

RESULT 14

US-10-415-724-3
; Sequence 3, Application US/10415724
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Prokinection Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: PP-UC 5030
; CURRENT APPLICATION NUMBER: US/10/415,724
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-724-3

Query Match 100.0%; Score 498; DB 30; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCGAGTCCCAISLMLRGLMCTPLGRGEGECHGSHKVPFFRRKRNHTCP 60
DB 1 AVITGACERDVOCGAGTCCCAISLMLRGLMCTPLGRGEGECHGSHKVPFFRRKRNHTCP 60
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86

RESULT 15

US-10-415-724A-3
; Sequence 3, Application US/10415724A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick J.
; TITLE OF INVENTION: Prokinection Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: 66778-316
; CURRENT APPLICATION NUMBER: US/10/415,724A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/245,882
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/47969
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-724A-3

Query Match 100.0%; Score 498; DB 30; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCGAGTCCCAISLMLRGLMCTPLGRGEGECHGSHKVPFFRRKRNHTCP 60

DB 1 AVITGACERDVOCGAGTCCCAISLMLRGLMCTPLGRGEGECHGSHKVPFFRRKRNHTCP 60
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86

Search completed: May 16, 2005, 07:02:11
Job time : 482 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:49:43 / Search time 48 Seconds
(without alignments)
190.162 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRPDPGRYRCSDMLKNINF 86

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 508155 seqs, 106137178 residues

Total number of hits satisfying chosen parameters: 177003

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	US-10-417-426A-9	Sequence 9, Appl
2	498	100.0	86	US-10-871-152-22	Sequence 22, Appl
3	498	100.0	86	US-10-503-554A-82	Sequence 82, Appl
4	498	100.0	86	US-11-048-649-9	Sequence 9, Appl
5	497	99.8	86	US-10-503-554A-81	Sequence 9, Appl
6	473	95.0	86	US-10-503-554A-138	Sequence 138, Appl
7	469	94.2	86	US-10-503-554A-142	Sequence 142, App
8	467	93.8	86	US-10-503-554A-140	Sequence 140, App
9	455	91.4	86	US-10-417-426A-10	Sequence 10, Appl
10	455	91.4	86	US-10-871-152-23	Sequence 23, Appl
11	455	91.4	86	US-10-503-554A-109	Sequence 109, Appl
12	455	91.4	86	US-11-048-649-10	Sequence 10, Appl
13	455	91.4	86	US-10-417-426A-21	Sequence 21, Appl
14	413	82.9	86	US-10-871-152-28	Sequence 28, Appl
15	413	82.9	86	US-11-048-649-21	Sequence 21, Appl
16	376	75.5	81	US-10-417-426A-20	Sequence 20, Appl
17	376	75.5	81	US-10-871-152-27	Sequence 27, Appl
18	376	75.5	81	US-11-048-649-20	Sequence 20, Appl
19	315	63.3	80	US-10-417-426A-13	Sequence 13, Appl
20	315	63.3	80	US-10-871-152-26	Sequence 26, Appl
21	315	63.3	80	US-10-503-554A-21	Sequence 21, Appl
22	315	63.3	80	US-11-048-649-13	Sequence 13, Appl
23	291	58.4	81	US-10-503-554A-22	Sequence 22, Appl
24	291	58.4	81	US-10-417-426A-5	Sequence 5, Appl
25	291	58.4	81	US-10-871-152-18	Sequence 18, Appl

26	291	58.4	81	6	US-10-503-554A-19	Sequence 19, Appl
27	291	58.4	81	7	US-11-048-649-5	Sequence 5, Appl
28	286	57.4	81	6	US-10-417-426A-7	Sequence 7, Appl
29	286	57.4	81	6	US-10-871-152-20	Sequence 20, Appl
30	286	57.4	81	6	US-10-503-554A-39	Sequence 39, Appl
31	286	57.4	81	7	US-11-048-649-7	Sequence 7, Appl
32	267.5	53.7	77	6	US-10-417-426A-11	Sequence 11, Appl
33	267.5	53.7	77	6	US-10-871-152-24	Sequence 24, Appl
34	267.5	53.7	77	6	US-11-048-649-11	Sequence 11, Appl
35	250.5	50.3	75	6	US-10-417-426A-12	Sequence 12, Appl
36	250.5	50.3	75	6	US-10-871-152-25	Sequence 25, Appl
37	250.5	50.3	75	6	US-11-048-649-12	Sequence 12, Appl
38	66	13.3	85	7	US-10-525-126-295	Sequence 295, App
39	60	12.0	74	8	US-60-669-241-37270	Sequence 37270, A
40	59.5	11.9	78	6	US-10-703-032-139163	Sequence 139163, A
41	58.5	11.7	84	5	US-09-999-570A-206	Sequence 206, App
42	58.5	11.7	84	5	US-09-992-600B-206	Sequence 206, App
43	58.5	11.7	84	6	US-10-001-142C-206	Sequence 206, App
44	58.5	11.7	84	6	US-10-000-986A-206	Sequence 206, App
45	58	11.6	65	6	US-10-450-763-49746	Sequence 49746, A

ALIGNMENTS

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RESULT 1
US-10-417-426A-9
; Sequence 9, Application US/10417426A
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Treating Circadian Rhythm Disorders
; FILE REFERENCE: 66778-309(UCS/773)
; CURRENT APPLICATION NUMBER: US/10/417,426A
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/372,836
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-426A-9

Query Match      100.0%; Score 498; DB 6; length 86;
Best Local Similarity 100.0%; Pred.No. 2.3e-48;
Matches      86; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 AVITGACERDVQCGAGTCCALSLWLRGLRMCTPLRGEGECHPSGHKVPFRKRKHHTCP 60
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DB      1 AVITGACERDVQCGAGTCCALSLWLRGLRMCTPLRGEGECHPSGHKVPFRKRKHHTCP 60
      |||||||

QY      61 CLPNLCSRPDPGRYRCSDMLKNINF 86
      |||||||
DB      61 CLPNLCSRPDPGRYRCSDMLKNINF 86
      |||||||

RESULT 2
US-10-871-152-22
; Sequence 22, Application US/10871152
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Novel Prokineticin Receptor Isoforms and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 66778-369
; CURRENT APPLICATION NUMBER: US/10/871,152
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/480,239
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 22
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
US-10-871-152-22

Query Match 100.0%; Score 498; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVOCAGTCCATISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKKHHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 3
US-10-503-554A-82
Sequence 82, Application US/10503554A

GENERAL INFORMATION:
APPLICANT: OHTAKI, TETSUYA
APPLICANT: MASUDA, YASUSHI
APPLICANT: TAKATSU, YOSHIHIRO
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
FILE REFERENCE: 61807 (46342)
CURRENT APPLICATION NUMBER: US/10/503,554A
CURRENT FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: JP2002-27299
PRIORITY FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 82
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
US-10-503-554A-82

Query Match 100.0%; Score 498; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVOCAGTCCATISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKKHHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 4
US-11-048-649-9
Sequence 9, Application US/11048649

GENERAL INFORMATION:
APPLICANT: Zhou, Qun-Yong
APPLICANT: Bullock, Clayton M.
TITLE OF INVENTION: Screening and Therapeutic Methods for
TITLE OF INVENTION: Treating Circadian Rhythm Disorders
FILE REFERENCE: 66778-317
CURRENT APPLICATION NUMBER: US/11/048,649
CURRENT FILING DATE: 2005-01-13
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
US-11-048-649-9

Query Match 100.0%; Score 498; DB 7; Length 86;

Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVOCAGTCCATISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKKHHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 5
US-10-503-554A-81
Sequence 81, Application US/10503554A

GENERAL INFORMATION:
APPLICANT: OHTAKI, TETSUYA
APPLICANT: MASUDA, YASUSHI
APPLICANT: TAKATSU, YOSHIHIRO
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
FILE REFERENCE: 61807 (46342)
CURRENT APPLICATION NUMBER: US/10/503,554A
CURRENT FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: JP2002-27299
PRIORITY FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 81
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
US-10-503-554A-81

Query Match 99.8%; Score 497; DB 6; Length 86;
Best Local Similarity 98.8%; Pred. No. 2.9e-48;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVOCAGTCCATISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKKHHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 6
US-10-503-554A-138
Sequence 138, Application US/10503554A

GENERAL INFORMATION:
APPLICANT: OHTAKI, TETSUYA
APPLICANT: MASUDA, YASUSHI
APPLICANT: TAKATSU, YOSHIHIRO
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
FILE REFERENCE: 61807 (46342)
CURRENT APPLICATION NUMBER: US/10/503,554A
CURRENT FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: JP2002-27299
PRIORITY FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 138
LENGTH: 86
TYPE: PRT
ORGANISM: Rattus sp.
US-10-503-554A-138

Query Match 95.0%; Score 473; DB 6; Length 86;
Best Local Similarity 91.9%; Pred. No. 1.4e-45;
Matches 79; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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DB 1 AVITGACERDVOCAGTCCATISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKKHHTCP 60

1 APPLICANT: OHTAKI, TETSUYA
 2 APPLICANT: MASUDA, YASUSHI
 3 APPLICANT: TAKATSU, YOSHIHIRO
 4 TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
 5 FILE REFERENCE: 61807 (46342)
 6 CURRENT APPLICATION NUMBER: US/10/503,554A
 7 CURRENT FILING DATE: 2004-08-04
 8 PRIOR APPLICATION NUMBER: JP2002-27299
 9 PRIOR FILING DATE: 2002-02-04
 10 NUMBER OF SEQ ID NOS: 184
 11 SOFTWARE: PatentIn Ver. 3.3
 12 SEQ ID NO 109
 13 LENGTH: 86
 14 TYPE: prt
 15 ORGANISM: Mus sp.
 16 US-10-503-554A-109

Query Match	91.4%	Score 455	DB 6	Length 86
Best Local Similarity	88.4%	Pred. No. 1.4e-43		
Matches 76	Conservative 5	Mismatches 5	Indels 0	Gaps 0

Dy 1 AVITGACERDVQCGAGTCCCAISLMLRGLMCTPLRGEGECHPGSHKVPFRXKRKHHTCP 60
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Db 1 AVITGACERDIQCGAGTCCCAISLMLRLPLTGRGEGECHPGSHKIPLPRKQHHTCP 60

OY 61 CLPNLLCSRFPPDGRYRCSDMLKINIF 86
| : | | | | | | | | |
Db 61 CSPSLTCSRFPDGRYRCFRDLKNANF 86

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RESULT 12
US-11-048-649-10
: Sequence 10, Application US/11048649
: GENERAL INFORMATION:
: APPLICANT: Zhou, Qun-Yong
: APPLICANT: Bullock, Clayton M.
: TITLE OF INVENTION: Screening and Therape
: TITLE OF INVENTION: Treating Citradian R
: FILE REFERENCE: 66778-317
: CURRENT APPLICATION NUMBER: US/11/048,649
: CURRENT FILING DATE: 2005-01-13
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 86
: TYPE: PRT
: ORGANISM: Mus musculus
US-11-048-649-10

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Query Match	91.4%	Score 455	DB 7	Length 86
Best Local Similarity	88.4%	Pred. NO. 1.4e-43		
Matches 76	Conservative 5	Mismatches 5	Indels 0	Gaps 0

QY 1 AVITGACERDVQCGAGTCCASIMLRGLMCTPLRGEGEECHPGSHKVPFRPKRKHNTP 66

Db 1 AVITGACERDVGCGAGTCCASIMLRGLRLCTPLRGEGEECHPGSHKIPFLRKQHNTP 66

Oy 61 CLPNLLCSRFPPDGRYRCMSMDLKNINF 86
 | : ||||| | | | | | | | |
Db 61 CSPSLLCSRFPDGRYRCFRDLKANVF 86

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RESULT 13
US-10-417-426A-21
: Sequence 21, Application US/10417426A
: GENERAL INFORMATION:
: APPLICANT: Zhou, Qun-Yong
: APPLICANT: Bullock, Clayton M.
: TITLE OF INVENTION: Screening and Therapeutic Methods For
: TITLE OF INVENTION: Treating Circadian Rhythm Disorders
: FILE REFERENCE: 66778-309(US5773)
: CURRENT APPLICATION NUMBER: US/10/417,426A
: CURRENT FILING DATE: 2003-04-15

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: PRIOR APPLICATION NUMBER: US 60/372,836
:
: PRIOR FILING DATE: 2003-04-15
:
: NUMBER OF SEQ ID NOS: 21
:
: SOFTWARE: FastSeq for Windows Version 4.0.
:
: SEQ ID NO 21
:
: LENGTH: 86
:
: TYPE: PRT
:
: ORGANISM: Artificial Sequence
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: FEATURE:
:
: OTHER INFORMATION: chimera
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: US-10-417-426A-21

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Query Match	82.9%;	Score	413;	DB	6;	length	86;
Best Local Similarity	76.7%;	Pred. No.	6.8e-39;				
Matches	66;	Conservative	12;	Mismatches	8;	Indels	0;
						Gaps	0;

QY 1 AVITGACERDYQCGAGTCCTCCALSMLRGLRMCTPLGREGECHPGSHKVPFFRRKRKHTTCTP 600

Db 1 AVITGACDKDSQCGGNCACVAISIWKSIRICTPMGLDPSCHPLTRKVPFFRRKRKHTTCTP 600

QY 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
Db 61 CLPNLLCSRFPDGRYRCMDLKNINF 86

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RESULT 14
US-10-871-152-28
: Sequence 28, Application US/10871152
: GENERAL INFORMATION:
: APPLICANT: Zhou, Qun-Yong
: TITLE OF INVENTION: Novel Prokineticin Receptor Isoforms and
: TITLE OF INVENTION: Methods of Use
: FILE REFERENCE: 66778-369
: CURRENT APPLICATION NUMBER: US/10/871,152
: CURRENT FILING DATE: 2004-06-18
: PRIOR APPLICATION NUMBER: 60/480,239
: PRIOR FILING DATE: 2003-06-20
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 28
: LENGTH: 86
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Chimera PK2/PK1
US-10-871-152-28

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Query Match	82.9%	Score 413	DB 36	length 86
Best Local Similarity	76.7%	Pred. NC. 6.8e-39		
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| | | | | : | | | | | : | | | | | : | | | | |
Db 1 AVITGACDKSQCGGGMCASIWVKSIRICTPMGLDSCHPILNRKVPEFRKRKHHTCP 600

OY	61	CLPNLLCSRFPDGRYRCMDLKNINF	86
Db	61	CLPNLLCSRFPDGRYRCMDLKNINF	86

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RESULT 15
US-11-048-649-21
: Sequence 21, Application US/11048649
: GENERAL INFORMATION:
: APPLICANT: Zhou, Qun-Yong
: APPLICANT: Bullock, Clayton M.
: TITLE OF INVENTION: Screening and Therapeutic Methods For
: TITLE OF INVENTION: Treating Circadian Rhythm Disorders
: FILE REFERENCE: 66778-317
: CURRENT APPLICATION NUMBER: US/11/048,649
: CURRENT FILING DATE: 2005-01-13
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FASTSEQ for Windows Version 4.0

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OM protein - protein search, using sw model

Run on: May 16, 2005, 06:44:33 ; Search time 43 Seconds
(without alignments)
149,298 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498
Sequence: 1 AVITGACERDVCGAGTCC...CSRFPDGRYRCMDLKNINF 86

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 312316

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	64.5	13.0	77	3 US-08-866-545-2	Sequence 2, App1
3	64.5	13.0	77	4 US-09-627-775-2	Sequence 2, App1
4	56.5	11.3	79	4 US-10-006-011A-7	Sequence 7, App1
5	55.5	11.1	44	1 US-08-050-319B-37	Sequence 37, App1
6	55.5	11.1	44	2 US-08-465-982-37	Sequence 37, App1
7	55.5	11.1	80	4 US-09-621-976-7198	Sequence 7198, App1
8	52.5	10.5	69	4 US-09-480-251-6	Sequence 6, App1
9	52.5	10.5	70	4 US-09-480-251-2	Sequence 2, App1
10	52	10.4	36	5 PCT-US96-01720-2	Sequence 2, App1
11	52	10.4	43	4 US-09-894-882-233	Sequence 233, App
12	52	10.4	43	4 US-09-894-882-260	Sequence 260, App
13	52	10.4	43	4 US-09-894-882-266	Sequence 266, App
14	52	10.4	43	4 US-09-894-882-272	Sequence 272, App
15	52	10.4	43	4 US-09-894-882-347	Sequence 347, App
16	51.5	10.3	74	4 US-09-270-767-34440	Sequence 34440, A
17	51.5	10.3	74	4 US-09-270-767-49657	Sequence 49657, A
18	51	10.2	43	4 US-09-894-882-483	Sequence 483, App
19	51	10.2	43	4 US-09-894-882-484	Sequence 484, App
20	51	10.2	43	4 US-09-894-882-487	Sequence 487, App
21	51	10.2	69	4 US-09-894-882-232	Sequence 232, App
22	51	10.2	69	4 US-09-894-882-259	Sequence 259, App
23	51	10.2	69	4 US-09-894-882-271	Sequence 271, App
24	50.5	10.1	72	4 US-09-270-767-41152	Sequence 41152, A
25	50.5	10.1	72	4 US-09-270-767-56368	Sequence 56368, A
26	50.5	10.1	77	1 US-08-264-534-1	Sequence 1, App1
27	50.5	10.1	77	1 US-08-083-590A-14	Sequence 14, App1

28	50.5	10.1	77	1 US-08-465-500-1	Sequence 1, App1
29	50.5	10.1	77	2 US-08-346-126-1	Sequence 1, App1
30	50.5	10.1	77	2 US-08-346-126-1	Sequence 1, App1
31	50.5	10.1	77	3 US-08-532-384-14	Sequence 14, App1
32	50.5	10.1	77	3 US-08-893-828-1	Sequence 1, App1
33	50	10.0	43	4 US-09-894-882-269	Sequence 269, App
34	50	10.0	43	4 US-09-894-882-485	Sequence 485, App
35	50	10.0	48	3 US-08-665-259-6	Sequence 6, App1
36	50	10.0	48	3 US-08-762-500-6	Sequence 6, App1
37	50	10.0	49	3 US-08-665-259-5	Sequence 5, App1
38	50	10.0	49	3 US-08-762-500-5	Sequence 5, App1
39	50	10.0	69	4 US-09-894-882-265	Sequence 265, App
40	50	10.0	70	4 US-09-894-882-353	Sequence 353, App
41	49.5	9.9	47	1 US-08-377-687-28	Sequence 28, App1
42	49.5	9.9	47	1 US-08-656-318A-13	Sequence 13, App1
43	49.5	9.9	47	2 US-08-777-192-28	Sequence 28, App1
44	49.5	9.9	47	2 US-08-956-459-13	Sequence 13, App1
45	49.5	9.9	47	3 US-08-971-982-28	Sequence 28, App1

ALIGNMENTS

RESULT 1
US-09-513-999C-4698
; Sequence 4698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Maline Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59. US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4698
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: score 7.2
; OTHER INFORMATION: seq VSIMILLVTVSDC/AV
US-09-513-999C-4698

Query Match
Best local similarity 98.4%; Pred. No. 1e-34;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATISLIRGLMCTPLRGEGEGCHPGSHKVPFRKKRKHHP 60
DB 20 AVITGACERDVCGAGTCCATISLIRGLMCTPLRGEGEGCHPGSHKVPFRKKRKHHP 79
QY 61 C 61
DB 80 C 80

RESULT 2
US-08-866-545-2
; Sequence 2, Application US/08866545
; Patent No. 6265535
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murail, Ramchandran
; APPLICANT: Takasaki, Wataru
; TITLE OF INVENTION: PEPTIDES AND PEPTIDE

TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAY-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009113-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265535e

US-08-866-545-2

Query Match 13.0%; Score 64.5; DB 3; Length 77;
Best Local Similarity 38.3%; Pred. No. 2.5;
Matches 18; Conservative 4; Mismatches 16; Indels 9; Gaps 3;

QY 2 VITGACERD---VQCGATCCALSLWRLGRLMCTPLGRGEECHPG 44
DB 32 VETQACTREQNRICTCRPGWYCALSK-QEGCRICAPL-----RKCRPG 73

RESULT 3
US-09-627-775-2
Sequence 2, Application US/09627775
Patent No. 6682739
GENERAL INFORMATION:
APPLICANT: Greene, Mark
APPLICANT: Murail, Ramachandran
APPLICANT: Aoki, Kazuhito
APPLICANT: Baron, Roland
TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
FILE REFERENCE: UPN3832
CURRENT APPLICATION NUMBER: US/09/627,775
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,090
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-627-775-2

Query Match 13.0%; Score 64.5; DB 4; Length 77;

Best Local Similarity 38.3%; Pred. No. 2.5;
Matches 18; Conservative 4; Mismatches 16; Indels 9; Gaps 3;

QY 2 VITGACERD---VQCGATCCALSLWRLGRLMCTPLGRGEECHPG 44
DB 32 VETQACTREQNRICTCRPGWYCALSK-QEGCRICAPL-----RKCRPG 73

RESULT 4
US-10-006-011A-7
Sequence 7, Application US/10006011A
Patent No. 6821947
GENERAL INFORMATION:
APPLICANT: Iozzo, Renato V.
TITLE OF INVENTION: Endorepellin: method and compositions
TITLE OF INVENTION: for inhibiting angiogenesis
FILE REFERENCE: 8321-95
CURRENT APPLICATION NUMBER: US/10/006,011A
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 79
TYPE: PRT
ORGANISM: human
US-10-006-011A-7

Query Match 11.3%; Score 56.5; DB 4; Length 79;
Best Local Similarity 30.3%; Pred. No. 22;
Matches 23; Conservative 4; Mismatches 36; Indels 13; Gaps 4;

QY 9 RDVQCGATCCALSLWRLGRLMCTPLGRGEECHPGSHKVPFRKRKHPCP--CLPNIL 66
DB 2 RDRPCQNGGCHDSESSSYVCV-PAGFTGRCE-----HSQALHCHPACGPDPAT 51
QY 67 CSRFPDGR-YRCMDL 81
DB 52 CVNRPDGRGYTCRCHL 67

RESULT 5
US-08-050-319B-37
Sequence 37, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M. Feldmann, P. W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 37;
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-319B-37

Query Match 11.1%; Score 55.5; DB 1; Length 44;
Best Local Similarity 40.6%; Pred. No. 15;
Matches 13; Conservative 3; Mismatches 11; Indels 5; Gaps 2;

Qy 13 CGAGTCCATSLWLRGLRMCTPLGRSEEGCHPG 44
Db 2 CRPGWYCALSK-QEGCRLCAPL-----RKCRPG 28

RESULT 6
US-08-465-982-37
Sequence 37, Application US/08465982
Patent No. 5863786

GENERAL INFORMATION:
APPLICANT: M. Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbings
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbings, Robert L.
REGISTRATION NUMBER: 33,208
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-982-37

Query Match 11.1%; Score 55.5; DB 2; Length 44;
Best Local Similarity 40.6%; Pred. No. 15;
Matches 13; Conservative 3; Mismatches 11; Indels 5; Gaps 2;

Qy 13 CGAGTCCATSLWLRGLRMCTPLGRSEEGCHPG 44
Db 2 CRPGWYCALSK-QEGCRLCAPL-----RKCRPG 28

RESULT 7

US-09-621-976-7198
Sequence 7198, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Joberc, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 7198
LENGTH: 80
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 74
OTHER INFORMATION: Xaa = *, Trp
US-09-621-976-7198

Query Match 11.1%; Score 55.5; DB 4; Length 80;
Best Local Similarity 29.4%; Pred. No. 30;
Matches 20; Conservative 6; Mismatches 29; Indels 13; Gaps 4;

Qy 9 KDVOGAGTCCATSLWLRGLRMCTPLGRSEEGCHPGSHKPPFRKRKHHTCPCLNLCS 68
Db 19 OSVFCSTSYCV-----LNTVPPI--EDHGNSSSHVKFLPKK--LLECLPK--CS 65

Qy 69 RPDGRYR 76
Db 66 SLPKRHR 73

RESULT 8
US-09-480-251-6
Sequence 6, Application US/09480251
Patent No. 6465719

GENERAL INFORMATION:
APPLICANT: Derose, Richard
APPLICANT: Freysinet, Georges
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant
FILE REFERENCE: A32889-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/480,251
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/FR98/01462
PRIOR FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: FRANCE 97/09,115
PRIOR FILING DATE: 1997-07-11
PRIOR APPLICATION NUMBER: FRANCE 9709,663
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 69
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The ubiquitin - drosomycin fusion peptide
US-09-480-251-6

Query Match 10.5%; Score 52.5; DB 4; Length 69;
Best Local Similarity 34.0%; Pred. No. 57;
Matches 16; Conservative 4; Mismatches 20; Indels 7; Gaps 3;

Qy 2 VITGACERDVOCGAGTC---CAISLWLRGL--RMCTPLGRSEEGCHP 43
Db 16 VVLGNADADCLSGRYKPCAV--WDNETCRVCKEGRSGSKHSP 60

RESULT 9
US-09-480-251-2
; Sequence 2, Application US/09480251
; Patent No. 6465719
; GENERAL INFORMATION:
; APPLICANT: Derose, Richard
; APPLICANT: Freysinet, Georges
; APPLICANT: Hofman, Jules
; TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
; TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant
; FILE REFERENCE: A32889-PCR-USA-A
; CURRENT APPLICATION NUMBER: US/09/480,251
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/FR98/01462
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: FRANCE 97/09,115
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: FRANCE 9709,663
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-480-251-2

Query Match 10.5%; Score 52.5; DB 4; Length 70;
Best Local Similarity 34.0%; Pred. No. 58;
Matches 16; Conservative 4; Mismatches 20; Indels 7; Gaps 3;

QY 2 VTGACERDVOCAGATC--CAISLWRLG--RMCPTPLGREGECBP 43
DB 17 VVIGANEADADCLSGRYKPCAV--WDETCTRVCKEGRSGHCSP 61

RESULT 10
PCT-US96-01720-2
; Sequence 2, Application PC/TUS9601720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,055
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE//DOCKET NUMBER: 16336-5PC
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-01720-2

Query Match 10.4%; Score 52; DB 5; Length 36;
Best Local Similarity 35.7%; Pred. No. 32;

Matches 15; Conservative 1; Mismatches 18; Indels 8; Gaps 2;

QY 4 TGACERDVOCAGATCCCAISLWRLGRLMCTPLGREGECBP 45
DB 3 TGAAGCAACG-GTCCAAC-----CCAGAGCGGTTCCAGA 36

RESULT 11
US-09-894-882-233
; Sequence 233, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 233
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Conus emaciatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(43)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residues 4 and 38
US-09-894-882-233

Query Match 10.4%; Score 52; DB 4; Length 43;
Best Local Similarity 33.3%; Pred. No. 39;
Matches 12; Conservative 2; Mismatches 14; Indels 8; Gaps 1;

QY 4 TGACERDVOCAGATCCCAISLWRLGRLMCTPLGREG 39
DB 5 TSXCRSFPCCGHCIC-----FRCSNSCRFGK 32

RESULT 12
US-09-894-882-260
; Sequence 260, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.


```
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 260
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Conus virgo
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residues 4 and 38
; OTHER INFORMATION: is Glu or gamma-carboxy-Gl
US-09-894-882-260
```

```
Query Match          10.4%; Score 52; DB 4; Length 43;
Best Local Similarity 33.3%; Pred. No. 39;
Matches 12; Conservative 2; Mismatches 14; Indels 8; Gaps 1;

QY      4 TGACERDVCGAGTCCCAISLWLRGLRMCTPLGREGE 39
Db       5 TSXCRSPQCCHGICCC-----FRCNSNCRFGK 32
```

```
RESULT 13
US-09-894-882-266
; Sequence 266, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 266
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Conus virgo
; FEATURE:
; NAME/KEY: PEPTIDE
```

```
; LOCATION: (1)..(43)
; OTHER INFORMATION: Xaa at residues 6 and 7 is Pro or hydroxy-Pro; Xaa at residues 4
; OTHER INFORMATION: and 38 is Glu or gamma-carboxy-Gl
US-09-894-882-266
```

```
Query Match          10.4%; Score 52; DB 4; Length 43;
Best Local Similarity 33.3%; Pred. No. 39;
Matches 12; Conservative 2; Mismatches 14; Indels 8; Gaps 1;

QY      4 TGACERDVCGAGTCCCAISLWLRGLRMCTPLGREGE 39
Db       5 TSXCRSPQCCHGICCC-----FRCNSNCRFGK 32
```

```
RESULT 14
US-09-894-882-272
; Sequence 272, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 272
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Conus virgo
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residues 4 and 38
; OTHER INFORMATION: is Glu or gamma-carboxy-Glu; Xaa at residue 3 is Tyr, 125i-Tyr, "
; OTHER INFORMATION: ono-lodo-Tyr, di-lodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
US-09-894-882-272
```

```
Query Match          10.4%; Score 52; DB 4; Length 43;
Best Local Similarity 33.3%; Pred. No. 39;
Matches 12; Conservative 2; Mismatches 14; Indels 8; Gaps 1;

QY      4 TGACERDVCGAGTCCCAISLWLRGLRMCTPLGREGE 39
Db       5 TSXCRSPQCCHGICCC-----FRCNSNCRFGK 32
```

```
RESULT 15
US-09-894-882-347
; Sequence 347, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
```

```

; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olvera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 347
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Conus striolatus
US-09-894-882-347

```

```

Query March 10.4%; Score 52; DB 4; Length 63;
Best Local Similarity 31.9%; Pred. No. 59;
Matches 15; Conservative 5; Mismatches 13; Indels 14; Gaps 3;

QY 2 VITACERDVCGAGTCCA-LSLWIRGLRMCTPLGRBGECHPSHK 47
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 VLTNACHMD--CSKWTCCSGICCFYCGRPMC-----PQTRR 52

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Search completed: May 16, 2005, 06:54:04
 Job time : 44 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:02 ; Search time 52 Seconds
(without alignments)
552.470 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCRSMIDKINIF 86

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 655

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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244	498	100.0	105	14	US-10-131-821A-470	Sequence 470, App	317	498	100.0	105	14	US-10-121-335-5	Sequence 5, Appl1
245	498	100.0	105	14	US-10-131-822A-470	Sequence 470, App	318	498	100.0	105	14	US-10-223-087-172	Sequence 172, App
246	498	100.0	105	14	US-10-131-828A-470	Sequence 470, App	319	498	100.0	105	14	US-10-132-157-2	Sequence 2, Appl1
247	498	100.0	105	14	US-10-131-835A-470	Sequence 470, App	320	498	100.0	105	14	US-10-127-886-470	Sequence 470, App
248	498	100.0	105	14	US-10-137-864A-470	Sequence 470, App	321	498	100.0	105	14	US-10-223-083-112	Sequence 172, App
249	498	100.0	105	14	US-10-137-869A-470	Sequence 470, App	322	498	100.0	105	14	US-10-216-166-166	Sequence 166, App
250	498	100.0	105	14	US-10-147-523-470	Sequence 470, App	323	498	100.0	105	14	US-10-223-612-166	Sequence 166, App
251	498	100.0	105	14	US-10-158-785-470	Sequence 470, App	324	498	100.0	105	14	US-10-223-089-112	Sequence 172, App
252	498	100.0	105	14	US-10-121-051-470	Sequence 470, App	325	498	100.0	105	14	US-10-137-866-470	Sequence 470, App
253	498	100.0	105	14	US-10-216-165-166	Sequence 166, App	326	498	100.0	105	14	US-10-146-726-470	Sequence 470, App
254	498	100.0	105	14	US-10-218-956-166	Sequence 166, App	327	498	100.0	105	14	US-10-146-727-470	Sequence 470, App
255	498	100.0	105	14	US-10-219-478-166	Sequence 166, App	328	498	100.0	105	14	US-10-146-788-470	Sequence 470, App
256	498	100.0	105	14	US-10-219-478-166	Sequence 166, App	329	498	100.0	105	14	US-10-153-380-470	Sequence 470, App
257	498	100.0	105	14	US-10-219-536-166	Sequence 166, App	330	498	100.0	105	14	US-10-153-934-470	Sequence 470, App
258	498	100.0	105	14	US-10-233-205-166	Sequence 166, App	331	498	100.0	105	14	US-10-140-807-470	Sequence 470, App
259	498	100.0	105	14	US-10-121-042-470	Sequence 166, App	332	498	100.0	105	14	US-10-140-924-470	

379	498	100.0	105	14	US-10-141-700-470	Sequence 470, App	452	498	100.0	105	14	US-10-147-520-470	Sequence 470, App
380	498	100.0	105	14	US-10-141-705-470	Sequence 470, App	453	498	100.0	105	14	US-10-157-781-470	Sequence 470, App
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384	498	100.0	105	14	US-10-142-420-470	Sequence 470, App	457	498	100.0	105	14	US-10-152-383-470	Sequence 470, App
385	498	100.0	105	14	US-10-142-422-470	Sequence 470, App	458	498	100.0	105	14	US-10-152-384-470	Sequence 470, App
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387	498	100.0	105	14	US-10-142-760-470	Sequence 470, App	460	498	100.0	105	14	US-10-152-389-470	Sequence 470, App
388	498	100.0	105	14	US-10-145-821-470	Sequence 470, App	461	498	100.0	105	14	US-10-152-390-470	Sequence 470, App
389	498	100.0	105	14	US-10-152-531-470	Sequence 166, App	462	498	100.0	105	14	US-10-152-392-470	Sequence 470, App
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392	498	100.0	105	14	US-10-142-761-470	Sequence 470, App	465	498	100.0	105	14	US-10-157-784-470	Sequence 470, App
393	498	100.0	105	14	US-10-142-763-470	Sequence 470, App	466	498	100.0	105	14	US-10-157-797-470	Sequence 470, App
394	498	100.0	105	14	US-10-142-765-470	Sequence 470, App	467	498	100.0	105	14	US-10-158-491-470	Sequence 470, App
395	498	100.0	105	14	US-10-142-887-470	Sequence 470, App	468	498	100.0	105	14	US-10-145-962-470	Sequence 470, App
396	498	100.0	105	14	US-10-142-888-470	Sequence 470, App	469	498	100.0	105	14	US-10-146-789-470	Sequence 470, App
397	498	100.0	105	14	US-10-143-034-470	Sequence 470, App	470	498	100.0	105	14	US-10-147-486-470	Sequence 470, App
398	498	100.0	105	14	US-10-143-116-470	Sequence 470, App	471	498	100.0	105	14	US-10-145-628-470	Sequence 470, App
399	498	100.0	105	14	US-10-144-951-470	Sequence 470, App	472	498	100.0	105	14	US-10-145-627-470	Sequence 470, App
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401	498	100.0	105	14	US-10-145-015-470	Sequence 470, App	474	498	100.0	105	14	US-10-145-962-470	Sequence 470, App
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405	498	100.0	105	14	US-10-145-630-470	Sequence 470, App	478	498	100.0	105	14	US-10-147-505-470	Sequence

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566	498	100.0	105	15	US-10-131-820A-470	Sequence 470, App
567	498	100.0	105	15	US-10-142-886-470	Sequence 470, App
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605	498	100.0	105	15	US-10-157-801-470	Sequence 470, App
606	498	100.0	105	15	US-10-157-882-470	Sequence 470, App
607	498	100.0	105	15	US-10-158-784-470	Sequence 470, App
608	498	100.0	105	15	US-10-158-789-470	Sequence 470, App
609	498	100.0	105	15	US-10-192-011-470	Sequence 470, App
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611	498	100.0	105	15	US-10-140-020-470	Sequence 470, App
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613	498	100.0	105	15	US-10-140-809-470	Sequence 470, App
614	498	100.0	105	15	US-10-140-865-470	Sequence 470, App
615	498	100.0	105	15	US-10-141-701-470	Sequence 470, App
616	498	100.0	105	15	US-10-141-754-470	Sequence 470, App
617	498	100.0	105	15	US-10-141-760-470	Sequence 470, App
618	498	100.0	105	15	US-10-142-485-470	Sequence 470, App
619	498	100.0	105	15	US-10-142-490-470	Sequence 470, App
620	498	100.0	105	15	US-10-143-113-470	Sequence 470, App
621	498	100.0	105	15	US-10-146-730-470	Sequence 470, App
622	498	100.0	105	15	US-10-146-792-470	Sequence 470, App
623	498	100.0	105	15	US-10-158-791-470	Sequence 470, App
624	498	100.0	105	15	US-10-156-843-470	Sequence 470, App
625	498	100.0	105	15	US-10-157-786-470	Sequence 470, App
626	498	100.0	105	15	US-10-152-405-470	Sequence 470, App
627	498	100.0	105	15	US-10-219-538-771	Sequence 371, App
628	498	100.0	105	15	US-10-147-558-470	Sequence 470, App
629	498	100.0	105	15	US-10-305-654-172	Sequence 172, App
630	498	100.0	105	15	US-10-232-226-166	Sequence 166, App
631	498	100.0	105	15	US-10-128-652A-470	Sequence 470, App
632	498	100.0	105	15	US-10-140-927-470	Sequence 470, App
633	498	100.0	105	15	US-10-230-130-166	Sequence 166, App
634	498	100.0	105	15	US-10-147-493-470	Sequence 470, App
635	498	100.0	105	15	US-10-145-127-470	Sequence 470, App
636	498	100.0	105	15	US-10-160-503-470	Sequence 470, App
637	498	100.0	105	15	US-10-143-118-470	Sequence 470, App
638	498	100.0	105	15	US-10-144-993-470	Sequence 470, App
639	498	100.0	105	15	US-10-158-787-470	Sequence 470, App
640	498	100.0	105	15	US-10-081-056-172	Sequence 172, App
641	498	100.0	105	15	US-10-219-535-166	Sequence 166, App
642	498	100.0	105	15	US-10-232-230-166	Sequence 166, App
643	498	100.0	105	15	US-10-140-024-470	Sequence 470, App
644	498	100.0	105	15	US-10-147-536-470	Sequence 470, App
645	498	100.0	105	15	US-10-333-132-23	Sequence 23, App1
646	498	100.0	105	15	US-10-119-480-166	Sequence 166, App
647	498	100.0	105	16	US-10-152-372-470	Sequence 470, App
648	498	100.0	105	16	US-10-680-755A-5	Sequence 5, App11
649	498	100.0	105	16	US-10-680-800A-5	Sequence 5, App11
650	498	100.0	105	17	US-10-931-886-470	Sequence 2, App1
651	498	100.0	105	17	US-10-811-338-2	Sequence 2, App1
652	498	100.0	105	17	US-10-912-297-2	Sequence 2, App1
653	498	100.0	105	17	US-10-692-299-2	Sequence 2, App1
654	498	100.0	105	17	US-10-158-788-470	Sequence 470, App
655	498	100.0	105	17	US-10-415-724-2	Sequence 2, App1

RESULT 1
US-10-016-481-3
; Sequence 3, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehliert, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016

RESULT 5-11-328-3
US-10-811-328-3
; Sequence 3, Application US/10811328
; Publication No. US20050026828A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion


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; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-811-328-3
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Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
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Db 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
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RESULT 6
US-10-912-907-3
; Sequence 3, Application US/10912907
; Publication No. US20050037464A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/912,907
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-912-907-3
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Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AVITGACERDVCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHGSHKVPFFRKRHHTCP 60
    |||
Db 1 AVITGACERDVCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHGSHKVPFFRKRHHTCP 60
    |||
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
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Db 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
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RESULT 7
US-10-415-724-3
; Sequence 3, Application US/10415724
; Publication No. US20050074758A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5030
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; CURRENT APPLICATION NUMBER: US/10/415,724
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-724-3
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Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AVITGACERDVCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHGSHKVPFFRKRHHTCP 60
    |||
Db 1 AVITGACERDVCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHGSHKVPFFRKRHHTCP 60
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QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
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Db 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
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RESULT 8
US-10-016-481-18
; Sequence 18, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-016-481-18
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Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 AVITGACERDVCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHGSHKVPFFRKRHHTCP 61
    |||
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
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Db 62 CLPNLLCSRFPPDGRYRCSDMLKNINF 87
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RESULT 9
US-10-323-157-18
; Sequence 18, Application US/10323157
; Publication No. US20030113867A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
```

```

; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-323-157-18

Query Match      100.0%; Score 498; DB 14; Length 87;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPSHKVPPFRKKKHTCP 60
    |||||||
DB 2 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPSHKVPPFRKKKHTCP 61

QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
    |||||||
DB 62 CLPNLCSRPDPGRYRCMDLKNINF 87

RESULT 10
US-10-811-328-18
; Sequence 18, Application US/10811328
; Publication No. US20050026828A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-811-328-18

Query Match      100.0%; Score 498; DB 17; Length 87;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPSHKVPPFRKKKHTCP 60
    |||||||
DB 2 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPSHKVPPFRKKKHTCP 61

QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
    |||||||
DB 62 CLPNLCSRPDPGRYRCMDLKNINF 87

RESULT 11
US-10-912-907-18
; Sequence 18, Application US/10912907
; Publication No. US20050037464A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
```

```

; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/912,907
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-912-907-18

Query Match      100.0%; Score 498; DB 17; Length 87;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPSHKVPPFRKKKHTCP 60
    |||||||
DB 2 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPSHKVPPFRKKKHTCP 61

QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
    |||||||
DB 62 CLPNLCSRPDPGRYRCMDLKNINF 87

RESULT 12
US-10-415-724-18
; Sequence 18, Application US/10415724
; Publication No. US20050074758A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: PP-UC 5030
; CURRENT APPLICATION NUMBER: US/10/415,724
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-415-724-18

Query Match      100.0%; Score 498; DB 17; Length 87;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPSHKVPPFRKKKHTCP 60
    |||||||
DB 2 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPSHKVPPFRKKKHTCP 61

QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
    |||||||
DB 62 CLPNLCSRPDPGRYRCMDLKNINF 87

RESULT 13
US-10-016-481-15
; Sequence 15, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
```

```

; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-10-016-481-15
```

```

Query Match          100.0%; Score 498; DB 13; Length 89;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
    |||||||
DB 4 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 63
    |||||||
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
    |||||||
DB 64 CLPNLLCSRFPPDGRYRCSDMLKNINF 89
    |||||||
```

RESULT 14

```

; US-10-323-157-15
; Sequence 15, Application US/10323157
; Publication No. US20030113867A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Zhout, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-10-323-157-15
```

```

Query Match          100.0%; Score 498; DB 14; Length 89;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
    |||||||
DB 4 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 63
    |||||||
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
    |||||||
DB 64 CLPNLLCSRFPPDGRYRCSDMLKNINF 89
    |||||||
```

```

RESULT 15
; US-10-811-328-15
; Sequence 15, Application US/10811328
; Publication No. US20050026828A1
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; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-10-811-328-15
```

```

Query Match          100.0%; Score 498; DB 17; Length 89;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
    |||||||
DB 4 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 63
    |||||||
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
    |||||||
DB 64 CLPNLLCSRFPPDGRYRCSDMLKNINF 89
    |||||||
```

```

Search completed: May 16, 2005, 08:22:03
Job time : 53 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:11:09 ; Search time 176 Seconds
(without alignments)
250.221 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVQCGAGTCGA.....CSRFPDGRYRCSMDKININP 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	105	1	PRK1_HUMAN
2	497	99.8	105	2	Q8TC69
3	473	95.0	105	1	PRK1_RAT
4	432	86.7	81	2	Q8K457
5	310.5	62.3	81	1	VPRA_DENPO
6	304	61.0	108	2	Q863H4
7	286	57.4	107	1	PRK2_RAT
8	284	57.0	128	2	Q863H5
9	278.5	55.9	96	2	Q8JFQ0
10	270.5	54.3	129	1	PRK2_HUMAN
11	267.5	53.7	96	1	BV8_BOMVA
12	265.5	53.3	128	1	PRK2_MOUSE
13	265.5	53.3	128	2	Q6V8U7
14	254.5	51.1	96	2	Q8JF66
15	253.5	50.9	96	2	Q8JF68
16	249.5	50.1	96	2	Q8JF69
17	249.5	50.1	96	2	Q8JF69
18	249.5	50.1	96	2	Q8JF69
19	246.5	49.5	96	2	Q8JF69
20	225.5	42.5	96	2	Q8JF69
21	108.5	21.8	221	2	Q8JF69
22	107.5	21.6	224	1	DKK4_HUMAN
23	107.5	21.6	350	1	DKK3_CHICK
24	104	20.9	255	2	Q9DDA4
25	102	20.5	259	1	DKK2_HUMAN
26	101	20.3	259	2	DKK2_MOUSE
27	101	20.3	259	2	Q8JF69
28	101	20.3	272	1	DKK1_MOUSE
29	101	20.3	272	2	Q8JF69
30	100.5	20.2	171	2	Q43532
31	100.5	20.2	215	2	Q8N294

32	100.5	20.2	350	1	DKK3_HUMAN	Q9ubp4 homo sapien
33	99.5	20.0	277	2	Q9ES33	Q9e33 rattus norv
34	98.5	19.8	349	1	DKK3_MOUSE	Q9gung mus musculu
35	97	19.5	266	1	DKK1_HUMAN	Q94307 homo sapien
36	96.5	19.4	268	2	Q6PV05	Q6pv05 oryctolagus
37	95.5	19.2	259	2	Q57464	Q57464 xenopus lae
38	94.5	19.0	350	2	Q6P081	Q6p081 homo sapien
39	94	18.9	240	2	Q9PWH3	Q9pwh3 brachydanto
40	88.5	17.8	640	2	Q96397	Q96397 chlamydomon
41	86	17.3	241	2	Q9M6D9	Q9m6d9 brachydanto
42	82.5	16.6	425	1	CND0_MOUSE	Q8bu04 mus musculu
43	82.5	16.6	425	2	Q642A8	Q642a8 rattus norv
44	81.5	16.4	446	2	Q8NB03	Q8nb03 homo sapien
45	81	16.3	1964	1	NTC4_MOUSE	P31695 mus musculu

ALIGNMENTS

RESULT 1
PRK1_HUMAN STANDARD; PRT; 105 AA.
ID PRK1_HUMAN
AC P58294;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial
DE growth factor) (EG-VEGF) (Mambakine) (UN0600/PRO1186).
GN Name=PROK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21160229; PubMed=11259612;
RA Li M., Bullock C.M., Knaier D.J., Ehler F.J., Zhou Q.Y.;
RT "Identification of two prokineticin cDNAs: recombinant proteins
RT potentially contract gastrointestinal smooth muscle.";
RL Mol. Pharmacol. 59:692-698(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21419730; PubMed=11528470; DOI=10.1038/35091000;
RA Lecouter J., Kowalski J., Foster J., Hass P., Zhang Z.,
RA Dillard-Telm L., Frantz G., Rangel L., Deguzman L., Keller G.-A.,
RA Peale F., Gurney A., Hillan K.J., Ferrara N.;
RT "Identification of an angiogenic mitogen selective for endocrine gland
RT endothelium.";
RL Nature 412:877-884(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Fraser C.;
RT "Mambakine", a snake venom related endocrine hormone that controls
RT macrophages.";
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wileand D., Woods K., Xie M.-H., Yanura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP SEQUENCE OF 20-34.

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RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -1- FUNCTION: Potentially contract gastrointestinal (GI) smooth muscle.
CC Induces proliferation, migration and fenestration (the formation
CC of membrane discontinuities) in capillary endothelial cells
CC derived from endocrine glands. Has little or no effect on a
CC variety of other endothelial and non-endothelial cell types.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary,
CC testis, adrenal and placenta.
CC -1- SIMILARITY: Belongs to the prokinectin family.
CC -----
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CC -----
DR EMBL; AF333024; AAK49918.1; -
DR EMBL; AY029225; AAK33111.1; -
DR EMBL; AY358683; AAK99046.1; -
DR HSSP; P25687; 11MT.
DR Genew; HGNC:18454; PROK1.
DR MIM; 606233; -
DR H-INVD; HIX0000868; -
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
DR KX Direct protein sequencing; Growth factor; Mitogen; Signal.
FT SIGNAL 1 19
FT CHAIN 20 105 Prokinectin 1.
FT DISULFID 26 38 By similarity.
FT DISULFID 32 50 By similarity.
FT DISULFID 37 78 By similarity.
FT DISULFID 60 86 By similarity.
FT DISULFID 80 96 By similarity.
SQ SEQUENCE 105 AA; 11715 MW; C7E3FDE30EFP416A CRC64;

Query Match 100.0%; Score 498; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 4,8e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQAGAGTCACISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKHHHTCP 60
DB 20 AVITGACERDVQAGAGTCACISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKHHHTCP 79
QY 61 CLPNLCSRPPDGRYRCMSMDLKNINF 86
DB 80 CLPNLCSRPPDGRYRCMSMDLKNINF 105

RESULT 2
Q8TC69 PRELIMINARY; PRT; 105 AA.
AC Q8TC69;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Prokinectin 1.
GN Name=PROK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Testis;
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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```

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bisak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hailton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025399; AAK25399.1; -
DR HSSP; P25687; 11MT.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
DR SEQUENCE 105 AA; 11729 MW; E570FDE30EFP52D2 CRC64;

Query Match 99.8%; Score 497; DB 2; Length 105;
Best Local Similarity 98.8%; Pred. No. 6.1e-45;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQAGAGTCACISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKHHHTCP 60
DB 20 AVITGACERDVQAGAGTCACISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKHHHTCP 79
QY 61 CLPNLCSRPPDGRYRCMSMDLKNINF 86
DB 80 CLPNLCSRPPDGRYRCMSMDLKNINF 105

RESULT 3
PRK1_RAT STANDARD; PRT; 105 AA.
ID PRK1_RAT;
AC Q8R414;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Prokinectin 1 precursor (Endocrine-gland-derived vascular endothelial
DE growth factor) (EG-VEGF).
GN Name=PROK1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley;
RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VEGF/prokinectins as cognate
RT ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
CC -1- FUNCTION: Potentially contract gastrointestinal (GI) smooth muscle.
CC Induces proliferation, migration and fenestration (the formation
CC of membrane discontinuities) in capillary endothelial cells
CC derived from endocrine glands. Has little or no effect on a
CC variety of other endothelial and non-endothelial cell types (By
CC similarity).

```

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the prokinectin family.

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CC EMBL; AY089983; AAM0104.1; -.
DR HSSP; P25687; 1IMT.
DR RGD; 620898; Prok1.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
KW Growth factor; Mitogen; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 105 Prokinectin 1.
FT DISULFID 26 38 By similarity.
FT DISULFID 32 50 By similarity.
FT DISULFID 37 78 By similarity.
FT DISULFID 60 86 By similarity.
FT DISULFID 80 96 By similarity.
SQ SEQUENCE 105 AA; 11642 MW; 8DF0C42122B1C5B6 CRC64;

Query Match Score 473; DB 1; Length 105;
Best Local Similarity 91.9%; Pred. No. 2.1e-42;
Matches 79; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVITACERDVCGAGTCCASISLMLRGLRMCTPLRGEGEGCHPGSHKVPFRKRKHHTCP 60
DB 20 AVITACERDVCGAGTCCASISLMLRGLRCLTPLRGEGEGCHPGSHKIPFRKRKHHTCP 79
61 CLPNLCSRFDPGRYRCSDMLKNINF 86
80 CSPSLCSRFDPGRYRCSDMLKNINF 105

RESULT 4
ID Q8K457 PRELIMINARY; PRT; 81 AA.
AC Q8K457;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DB Prokinectin 1 (Fragment).
GN Name=Prok1; Synonyms=Pkl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bernack J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.Y.;
RT "Prokinectin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410 (2002).
DR EMBL; AF487281; AA049573.1; -.
DR HSSP; P25687; 1IMT.
DR MGD; MGI:2180370; Prok1.
DR GO; GO:0005576; Cytoplasmic; IDA.
DR GO; GO:000187; Proliferation of MAPK; IDA.
DR GO; GO:0007623; Proliferation of MAPK; IDA.
DR GO; GO:0008284; Proliferation of MAPK; IDA.
DR GO; GO:0045765; Proliferation of MAPK; IDA.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
FT NON TER 1 1
SQ SEQUENCE 81 AA; 9192 MW; 7BBE3EC6B16A011 CRC64;

Query Match Score 432; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 3.5e-38;
Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 ACERDVCGAGTCCASISLMLRGLRMCTPLRGEGEGCHPGSHKVPFRKRKHHTCCLNLT 65
DB 1 ACERDVCGAGTCCASISLMLRGLRCLTPLRGEGEGCHPGSHKIPFRKRKHHTCCLNLT 60
66 LCSRDPGRYRCSDMLKNINF 86
61 LCSRDPGRYRCSDMLKNINF 81

RESULT 5
ID VERA_DENPO STANDARD; PRT; 81 AA.
AC P25687;
DT 01-MAY-1992 (Rel. 22, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Intestinal toxin 1 (MIT 1) (MIT1) (Venom protein A).
OS Dendroaspis polylepsis polylepsis (Black mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OX NCBI_TaxID=8620;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=8115818; PubMed=7461607;
RA Joubert F.J., Stridom D.J.;
RT "Snake venom. The amino acid sequence of protein A from Dendroaspis
RT polylepsis polylepsis (black mamba) venom.";
RL Hope-Seyler's Z. Physiol. Chem. 361:1787-1794 (1980).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
RA Schweitz H., Pascaud P., Diocot S., Moliner D., Lazdunski M.;
RT "MIT1, a black mamba toxin with a new and highly potent activity on
RT intestinal contraction.";
RL FEBS Lett. 461:183-188 (1998).
RN [3]
RP STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
RA Boudouvier J., Albrand J.-P., Blackledge M., Jaquinod M.,
RA Schweitz H., Lazdunski M., Moliner D.;
RT "A structural homologue of colipase in black mamba venom revealed by
RT NMR floating disulphide bridge analysis.";
RL J. Mol. Biol. 283:205-219 (1998).
CC -1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the prokinectin family.
DR PDB; 1IMT; NMR; @=1-81.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
KW 3D-structure; Direct protein sequencing; Toxin.
FT DISULFID 7 19
FT DISULFID 13 31
FT DISULFID 18 60
FT DISULFID 41 68
FT DISULFID 62 78
FT DISULFID 73 73
FT VARIANT 73 73 P -> Q (in protein A').
FT CONFLICT 18 18 C -> S (in Ref. 1).
FT CONFLICT 22 22 S -> C (in Ref. 1).
SQ SEQUENCE 81 AA; 8645 MW; 6C01368841572044 CRC64;

Query Match Score 310.5; DB 1; Length 81;
Best Local Similarity 62.8%; Pred. No. 2.4e-25;
Matches 49; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 1 AVITACERDVCGAGTCCASISLMLRGLRMCTPLRGEGEGCHPGSHKVPFRKRKHHTC 59

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Db      1 AVITGACERDLOQCGKGCACAVSLWIKSVRCPTVGTSGECHOHPASHKIPFGSGRKHHTC 60
QY      60 PCLEPNLCSRPDPGRYRC 77
Db      61 PCAPNLACVQTSPPKRC 78

RESULT 6
0863H4  PRELIMINARY; PRT; 108 AA.
ID      0863H4
AC      0863H4
DT      01-JUN-2003 (TREMBlrel. 24, Created)
DT      01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE      Bv8/prokineticin 2-like protein splice variant.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RX      MEDLINE=2612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
RA      Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;
RT      "The AVIT protein family.";
RL      EMBL; AY192558; AAP31907.1; -.
DR      HSSP; P25687; 11MT.
DR      InterPro; IPR009523; Prokineticin.
DR      Pfam; PF06607; Prokineticin; 1.
SQ      SEQUENCE 108 AA; 11672 MW; C0041039A9B215E CRC64;

Query Match      61.0%; Score 304; DB 2; Length 108;
Best Local Similarity 62.3%; Pred. No. 1.6e-24;
Matches 48; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY      1 AVITGACERDVOCAGTCCATSLWLRGLRMCTPLGRGEGCHGSHKVPFRKRKHHTCP 60
Db      28 AVITGACDRDPQCGGCGCAVSLWIKSVIRICTPWGKVGDSCHPLTRKVPFGRRMHHTCP 87

QY      61 CLEPNLCSRPDPGRYRC 77
Db      88 CLPGLACSRTPFNRYTC 104

RESULT 7
PRK2_RAT  STANDARD; PRT; 107 AA.
ID      086413;
AC      086413;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Prokineticin 2 precursor (PK2).
GN      Name=Prok2; Synonyms=Bv8;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley;
RX      MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA      Masuda Y., Takatsu Y., Tetso Y., Kumano S., Ishibashi Y., Suenaga M.,
RA      Aoe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA      Inatomi N., Ohteki T., Onda H., Fujino M.;
RT      "Isolation and identification of EG-VEGF/prokineticins as cognate
RT      ligands for two orphan G-protein-coupled receptors.";
RL      Biochem. Biophys. Res. Commun. 293:396-402(2002).
RN      [2]
RP      EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
RX      MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;

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RA      Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bemark J.C., Belluzzi J.,
RA      Weaver D.R., Leslie F.M., Zhou O.-Y.;
RT      "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT      suprachiasmatic nucleus.";
RL      Nature 417:405-410(2002).
CC      -1- FUNCTION: May function as an output molecule from the
CC      suprachiasmatic nucleus (SCN) that transmits behavioural circadian
CC      rhythm. May also function locally within the SCN to synchronize
CC      output. Potently contracts gastrointestinal (GI) smooth muscle (By
CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC      -1- TISSUE SPECIFICITY: Expressed at high levels in testis and at
CC      lower levels in brain, lung, ovary, spleen, thymus and uterus.
CC      -1- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
CC      inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC      genes (CRY1 and CRY2) (Probable).
CC      -1- SIMILARITY: Belongs to the prokineticin family.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AY089984; AAM09105.1; -.
DR      HSSP; P25687; 11MT.
DR      RGD; 620280; Bv8.
DR      InterPro; IPR009523; Prokineticin.
DR      Pfam; PF06607; Prokineticin; 1.
KM      Biological rhythms; Neuropeptide; Signal.
FT      SIGNAL 1 26 Potential.
FT      CHAIN 1 107 Prokineticin 2.
FT      DISULFID 33 45 By similarity.
FT      DISULFID 39 57 By similarity.
FT      DISULFID 44 85 By similarity.
FT      DISULFID 67 93 By similarity.
FT      DISULFID 87 103 By similarity.
SQ      SEQUENCE 107 AA; 11594 MW; BDF316DCD5FED0 CRC64;

Query Match      57.4%; Score 286; DB 1; Length 107;
Best Local Similarity 57.1%; Pred. No. 1.2e-22;
Matches 44; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY      1 AVITGACERDVOCAGTCCATSLWLRGLRMCTPLGRGEGCHGSHKVPFRKRKHHTCP 60
Db      27 AVITGACDRDPQCGGCGCAVSLWIKSVIRICTPWGKVGDSCHPLTRKVPFGRRMHHTCP 86

QY      61 CLEPNLCSRPDPGRYRC 77
Db      87 CLPGLACSRTPFNRYTC 103

RESULT 8
0863H5  PRELIMINARY; PRT; 128 AA.
ID      0863H5;
AC      0863H5;
DT      01-JUN-2003 (TREMBlrel. 24, Created)
DT      01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE      Bv8/prokineticin 2-like protein.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RX      MEDLINE=2612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
RA      Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;
RT      "The AVIT protein family.";

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RL EMOB Rep. 4:469-473(2003).
 DR EMBL: AY192557; AAP31906.1; -.
 DR HSSP: P25687; 11MT.
 DR GO: GO:0005576; C.eitracellular; ISS.
 DR GO: GO:0001664; F-G-protein-coupled receptor binding; ISS.
 DR GO: GO:000187; P-activation of MAPK; ISS.
 DR GO: GO:0001525; P-angiogenesis; ISS.
 DR GO: GO:0006916; P-anti-apoptosis; ISS.
 DR GO: GO:0008283; P-cell proliferation; ISS.
 DR GO: GO:0006935; P-chemotaxis; ISS.
 DR GO: GO:0007204; P-cytosolic calcium ion concentration elevation; ISS.
 DR GO: GO:0007186; P-G-protein coupled receptor protein signalin. . .; ISS.
 DR GO: GO:0006954; P-inflammatory response; ISS.
 DR GO: GO:0019233; P-perception of pain; ISS.
 DR GO: GO:0045987; P-positive regulation of smooth muscle contra. . .; ISS.
 DR GO: GO:0007283; P-spermatogenesis; ISS.
 DR InterPro: IPR009523; Prokineticin.
 DR Pfam: PF06607; Prokineticin; 1.
 SQ SEQUENCE 128 AA; 14290 MW; C22CDBDE40483EC CRC64;

Query Match 57.0%; Score 284; DB 2; Length 128;
 Best Local Similarity 49.5%; Pred. No. 2, 4e-22;
 Matches 48; Conservative 11; Mismatches 18; Indels 20; Gaps 1;

QY 1 AVITGACERDVOCAGTCCASISLMLRLGMLCTPLGREGEGCHPGSH-----46
 DB 28 AVITGACERDVOCAGTCCASISLMLRLGMLCTPLGREGEGCHPGSH-----46

QY 47 -----KVPFRKRKHHTCPCLPMLCSRPDGRYC 77
 DB 88 KRRKKKVPFLGRMHHTCPCLPGLCSRTSFRKYC 124

RESULT 9
 Q8JF00 PRELIMINARY; PRT; 96 AA.
 ID 08JF00;
 AC TISSUE=Skin secretions;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 OS Bv8 protein homolog 2.
 DE Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
 CC NCB1_Taxid=161274;
 CX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin secretions;
 RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
 RA Lai R., Liu H., Lee W.H., Zhang Y.
 RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina maxima".
 RT Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
 DR EMBL: AF411091; AN03822.1; -.
 DR HSSP: P25687; 11MT.
 DR InterPro: IPR009523; Prokineticin.
 DR Pfam: PF06607; Prokineticin; 1.
 SQ SEQUENCE 96 AA; 10198 MW; EC4EAA5EFE49B2FO CRC64;

Query Match 55.9%; Score 278.5; DB 2; Length 96;
 Best Local Similarity 61.5%; Pred. No. 6, 9e-22;
 Matches 48; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 AVITGACERDVOCAGTCCASISLMLRLGMLCTPLGREGEGCHPGSHKVPFRKRKHHTCP 60
 DB 20 AVITGACERDVOCAGTCCASISLMLRLGMLCTPLGREGEGCHPGSHKVPFRKRKHHTCP 60
 QY 61 CLPMLCSRPDGRYCS 78
 DB 80 CKSGLTCSKSGE-KFQCS 96

RESULT 10

PRK2 HUMAN
 ID PRK2 HUMAN STANDARD; PRT; 129 AA.
 AC Q9HC23;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Prokineticin 2 precursor (PRK2) (Protein Bv8 homolog).
 GN Name=PROK2; Synonyms=Bv8;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCB1_Taxid=9606;
 CX [1]
 RP SEQUENCE OF 5-129 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RX MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8;
 RA Wechsleber C., Puglisi R., Leppendinger G., Boliani C., Kreil G.,
 RT "The mammalian homolog of Bv8 from frog skin is mainly expressed in
 RT spermatocytes".
 RL FEBS Lett. 462:177-181(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=21160229; PubMed=11259612;
 RA Li M., Bullock C.M., Knaier D.J., Ehler F.J., Zhou Q.-Y.;
 RT "Identification of two prokineticin cDNAs: recombinant proteins
 RT potentially contract gastrointestinal smooth muscle".
 RL Mol. Pharmacol. 59:692-698(2001).
 RN [3]
 RP SEQUENCE OF 28-42.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites".
 RL Protein Sci. 13:2819-2824(2004).
 CC -1- FUNCTION: May function as an output molecule from the
 CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
 CC rhythm. May also function locally within the SCN to synchronize
 CC output. Potentially contracts gastrointestinal (GI) smooth muscle.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9HC23-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9HC23-2; Sequence=VSP_005219;
 CC -1- TISSUE SPECIFICITY: Expressed in the testis and, at low levels, in
 CC the small intestine.
 CC -1- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
 CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
 CC genes (CRY1 and CRY2) (Probable).
 CC -1- SIMILARITY: Belongs to the prokineticin family.
 CC -----
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 CC -----
 DR EMBL: AF182069; AAG16893.2; -.
 DR EMBL: AF333025; AAK49919.1; -.
 DR HSSP: P25687; 11MT.
 DR Genew: HGNC:18455; PROK2.
 DR MIM: 607002; -.
 DR GO: GO:0005576; C.eitracellular; TAS.
 DR GO: GO:0001664; F-G-protein-coupled receptor binding; TAS.
 DR GO: GO:000187; P-activation of MAPK; TAS.
 DR GO: GO:0001525; P-angiogenesis; IDA.
 DR GO: GO:0006916; P-anti-apoptosis; IDA.
 DR GO: GO:0008283; P-cell proliferation; IDA.
 DR GO: GO:0006935; P-chemotaxis; IDA.
 DR GO: GO:0007204; P-cytosolic calcium ion concentration elevation; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . NAS.
 DR GO; GO:0006954; P:inflammatory response; NAS.
 DR GO; GO:0019233; P:perception of pain; TAS.
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . . ; IDA.
 DR GO; GO:0007283; P:spermatogenesis; IMP.
 DR Pfam; PF06607; Prokineticin; 1.
 DR Alternative splicing; Biological rhythms; Direct protein sequencing;
 KM Neuropeptide; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 129 Prokineticin 2.
 FT DISULFID 34 46 By similarity.
 FT DISULFID 40 58 By similarity.
 FT DISULFID 45 107 By similarity.
 FT DISULFID 68 115 By similarity.
 FT DISULFID 109 125 By similarity.
 FT VARSPIC 75 95 Missing (in isoform 2).
 FT FTid=VSP_005219.
 SQ SEQUENCE 129 AA; 14314 MW; 0487679E8700DA55 CRC64;
 Query Match 54.3%; Score 270.5; DB 1; Length 129;
 Best Local Similarity 45.9%; Pred. No. 6.5e-21; Indels 21; Gaps 1;
 Matches 45; Conservative 14; Mismatches 18;
 QY 1 AVITGACRDVQAGTCCATSLMRLGRLMCTPLRGEGEBCHPGSHK-----47
 DB 28 AVITGACDQKSGCGGCAVSIWKSIRICTPFGKLGDSCHPLTRKNNGNGRKRK 87
 QY 48 -----VPPFRKRKHTCPCLPNLICSPPDGRYRC 77
 DB 88 KRSKRKKEVPFGRMRHHTCPCLPGIACLRISFNRFLIC 125
 RESULT 11
 BV8_BOMVA STANDARD; PRT; 96 AA.
 ID BV8_BOMVA
 AC Q9PWE6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein Bv8 precursor.
 OS Bombina variegata (Yellow-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
 ON NCBI_Taxid=8348;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=9349621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0;
 RA Molloy C., Wechseltberger C., Mignogna G., Negri L., Melchiorri P.,
 RA Barra D., Kreil G.;
 RT "Bv8, a small protein from frog skin and its homologue from snake
 RT venom induce hyperalgesia in rats."
 RL Eur. J. Pharmacol. 374:189-196(1999).
 CC -1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
 CC -1- INDUCES hyperalgesia.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the prokineticin family.
 CC -----
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 CC -----
 CC EMBL; AF168790; AAD45816.1; .
 DR HSSP; P25687; 1IMT.
 DR InterPro; IPR009523; Prokineticin.
 DR Pfam; PF06607; Prokineticin; 1.
 KM Direct protein sequencing; Signal.
 FT SIGNAL 1 19

FT CHAIN 20 96 Protein Bv8.
 FT DISULFID 26 38 By similarity.
 FT DISULFID 32 50 By similarity.
 FT DISULFID 37 78 By similarity.
 FT DISULFID 60 86 By similarity.
 FT DISULFID 80 95 By similarity.
 SQ SEQUENCE 96 AA; 10102 MW; A12490A7437609B4 CRC64;
 Query Match 53.7%; Score 267.5; DB 1; Length 96;
 Best Local Similarity 57.7%; Pred. No. 1e-20; Indels 1; Gaps 1;
 Matches 45; Conservative 11; Mismatches 21;
 QY 1 AVITGACRDVQAGTCCATSLMRLGRLMCTPLRGEGEBCHPGSHKVPFRKRKHTCP 60
 DB 20 AVITGACDQKSGCGGCAVSIWKSIRICTPFGKLGDSCHPLTRKNNGNGRKRK 79
 QY 61 CLPNLICSPPDGRYRC 78
 DB 80 CKSGLTCKSGE-KFKCS 96
 RESULT 12
 PRK2_MOUSE STANDARD; PRT; 128 AA.
 ID PRK2_MOUSE
 AC Q9QXU7; Q9QXU5; Q9QXU6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Prokineticin 2 precursor (PK2) (Protein Bv8 homolog).
 GN Name=PRK2; Synonyms=Bv8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=129/Sv;
 RX MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8;
 RA Wechseltberger C., Puglisi R., Lepperdinger G., Bolteni C., Kreil G.;
 RT "The mammalian homologue of Bv8 from frog skin is mainly expressed in
 RT spermatocytes."
 RL FEBS Lett. 462:177-181(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
 RC STRAIN=129/Sv;
 RX PubMed=11054548; DOI=10.1016/S0378-1119(00)00355-3;
 RA Ullik A., Engel E., Beier D., Lepperdinger G.;
 RT "Murine Bv8 gene maps near a syntenic breakpoint of mouse chromosome 6
 RT and human 3p21."
 RL Gene 256:189-195(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND FUNCTION.
 RC STRAIN=C57BL/6;
 RX MEDLINE=22022114; PubMed=12024206; DOI=10.1038/417405a;
 RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bertini J.C., Belluzzi J.,
 RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
 RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
 RT suprachiasmatic nucleus."
 RL Nature 417:405-410(2002).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354663; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batilov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan M.J., Pereira G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Seton M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda K.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kawata I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT Nature 420:563-573 (2002)."
RL 60,770 full-length cDNAs."
CC -1- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potently contracts gastrointestinal (GI) smooth muscle (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Bv8-a;
CC IsoId=Q9QXU7-1; Sequence=Displayed;
CC Name=2; Synonyms=Bv8-b;
CC IsoId=Q9QXU7-2; Sequence=VSP_005220;
CC Name=3;
CC IsoId=Q9QXU7-3; Sequence=VSP_005221;
CC -1- TISSUE SPECIFICITY: Expressed in the SCN and among a few other
CC discrete brain areas, including the islands of Calleja, media I
CC preoptic area of the hypothalamus and the shell of the nucleus
CC accumbens. Highly expressed in testis. In the SCN, expression
CC subjected to high amplitude of circadian oscillation.
CC -1- DEVELOPMENTAL STAGE: Expressed in mid-late pachytene spermatocytes
CC at the stages VII, VIII and IX of the semiterous epithelial cycle.
CC -1- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC genes (CRY1 and CRY2).
CC -1- SIMILARITY: Belongs to the prokinectin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF182064; AAF15259.1; -;
CC EMBL; AF182065; AAF15260.1; -;
CC EMBL; AF182066; AAF15261.1; -;
CC EMBL; AF182068; AAG09439.1; -;
CC EMBL; AF182067; AAG09439.1; JOINED.
CC EMBL; AF487280; AAM49572.1; -;
CC EMBL; AK015462; BAB29857.1; -;
CC HSSP; P25687; 11MT.
CC MGD; MG1:1354178; Prok2.
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0001664; F:G-protein-coupled receptor binding; ISS.
CC GO; GO:000187; P:activation of MAPK; ISS.
CC GO; GO:0001525; P:angiogenesis; ISS.
CC GO; GO:0006916; P:anti-apoptosis; ISS.
CC GO; GO:0008283; P:cell proliferation; ISS.
CC GO; GO:0006933; P:chemotaxis; ISS.
CC GO; GO:0007623; P:circadian rhythm; IDA.
CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; ISS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; ISS.
CC GO; GO:0006954; P:inflammatory response; ISS.

DR GO; GO:0019233; P:perception of pain; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. .; ISS.
DR GO; GO:0007283; P:spermatogenesis; ISS.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
KW Alternative splicing; Biological rhythms; Neuropeptide; signal.
FT SIGNAL
FT CHAIN 1 26
FT DISULFID 27 128 Prokinectin 2.
FT DISULFID 33 45 By similarity.
FT DISULFID 39 57 By similarity.
FT DISULFID 44 106 By similarity.
FT DISULFID 67 114 By similarity.
FT DISULFID 108 124 By similarity.
FT VARSPPLIC 74 94 Missing (in isoform 2).
FT VARSPPLIC 74 128 /FTId=VSP_005220.
FT VARSPPLIC 74 128 SHVANGROEERRAKRRKKKVFWRGRRMHTCPCLPGLAC
FT LRTSFNRFCILARK -> VSVCTGILVPSH (in
FT isoform 3).
FT FTId=VSP_005221.
FT FTId=VSP_005220.
SQ SEQUENCE 128 AA; 14185 MW; 5F08BA177EDDB58C CRC64;
Query Match 53.3%; Score 265.5; DB 1; Length 128;
Best Local Similarity 44.9%; Pred. No. 2.2e-20;
Matches 44; Conservative 15; Mismatches 18; Indels 21; Gaps 1;
QY 1 AVITGACRDVOCGAGTCCATSLMRLGRLMCTPLGREGEECHPGSHK----- 47
DB 27 AVITACDDSDCGGMCACAVSIWKSIRICTPLMGQVDSCHPLTRKSHVANGROERRA 86
QY 48 -----VPEFRKKKHTCPCLPMILCSRPDPGRYRC 77
DB 87 KRRKKKEVPFWRGRRMHTCPCLPGLACLRISFNNFIC 124
RESULT 13
QY 06V8J7 PRELIMINARY; PRT; 128 AA.
AC 06V8J7;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Prokinectin 2 beta.
GN Name=PK2beta;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Chen J., Sutton S., Kuei C., Wilson S.J., Lovenberg T.W., Liu C.;
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY348322; AAR06924.1; -;
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
SQ SEQUENCE 128 AA; 14223 MW; 67050CC1A7D59466 CRC64;
Query Match 53.3%; Score 265.5; DB 2; Length 128;
Best Local Similarity 44.9%; Pred. No. 2.2e-20;
Matches 44; Conservative 15; Mismatches 18; Indels 21; Gaps 1;
QY 1 AVITGACRDVOCGAGTCCATSLMRLGRLMCTPLGREGEECHPGSHK----- 47
DB 27 AVITACDDSDCGGMCACAVSIWKSIRICTPLMGQVDSCHPLTRKSHVANGROERRA 86
QY 48 -----VPEFRKKKHTCPCLPMILCSRPDPGRYRC 77
DB 87 KRRKKKEVPFWRGRRMHTCPCLPGLACLRISFNNFIC 124
RESULT 14
QY 06V8J7 PRELIMINARY; PRT; 96 AA.
ID Q6JFE6

AC Q8JFE6: 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bm8-a protein precursor (Bv8 protein homolog 1).
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Farragher S., Bjourson A.U., Orr D.F., Rao P., Shaw C.;
RT "granular gland transcriptomes in stimulated amphibian skin
RT secretions.", 371:125-130(2003).
RL U. Biochem. 371:125-130(2003).
RT [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin secretions;
RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
RA Lai R., Liu H., Lee W.H., Zhang Y.;
RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina
RT maxima".
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
DR EMBL; AJ440230; CAD29340.1; -.
DR EMBL; AF411090; AAN03821.1; -.
DR HSSP; P25687; 1MT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KM Signal.
FT CHAIN 1 19 Potential.
SQ SEQUENCE 96 AA; 10117 MW; 2269AAC654B18A6 CRC64; Bm8-a protein.
Query Match 51.1%; Score 254.5; DB 2; Length 96;
Best Local Similarity 56.4%; Pred. No. 2.4e-19;
Matches 44; Conservative 10; Mismatches 23; Indels 1; Gaps 1;
QY 1 AVITGACERDVOCGAGTCCATISLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 60
DB 20 AVITGVCDRDAQCGSGTCCASAFSRNIRFCVPLGNNGECPASHKVPYNGKRLSSICP 79
QY 61 CLPNLCSRFPPDGRYRCS 78
DB 80 CNTGLTCKSKGE-KFGCS 96
RESULT 15
Q8JFE6
ID Q8JFE6 PRELIMINARY; PRT; 96 AA.
AC Q8JFE6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Bm8-f protein precursor.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Farragher S., Bjourson A.U., Orr D.F., Rao P., Shaw C.;
RT "granular gland transcriptomes in stimulated amphibian skin
RT secretions.", 371:125-130(2003).
RL U. Biochem. 371:125-130(2003).
RT [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
RA Lai R., Liu H., Lee W.H., Zhang Y.;
RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina
RT maxima".
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
DR EMBL; AJ440230; CAD29340.1; -.
DR EMBL; AF411090; AAN03821.1; -.
DR HSSP; P25687; 1MT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KM Signal.
FT CHAIN 1 19 Potential.
SQ SEQUENCE 96 AA; 10117 MW; 2269AAC654B18A6 CRC64; Bm8-f protein.

SQ SEQUENCE 96 AA; 10058 MW; 2269A070FE118A6 CRC64;
Query Match 50.9%; Score 253.5; DB 2; Length 96;
Best Local Similarity 57.7%; Pred. No. 3e-19;
Matches 45; Conservative 8; Mismatches 24; Indels 1; Gaps 1;
QY 1 AVITGACERDVOCGAGTCCATISLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 60
DB 20 AVITGVCDRDAQCGSGTCCASAFSRNIRFCVPLGNNGECPASHKVPYNGKRLSSICP 79
QY 61 CLPNLCSRFPPDGRYRCS 78
DB 80 CNTGLTCKSKGE-KYQCS 96
Search completed: May 16, 2005, 06:34:28
Job time : 180 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: May 16, 2005, 08:10:07 ; Search time 162 Seconds
(without alignments)
205.317 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCSDMKINIF 86

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 420

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%
Listing first 500 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq19806:*
2: geneseq19906:*
3: geneseq20006:*
4: geneseq20016:*
5: geneseq20026:*
6: geneseq20036:*
7: geneseq20046:*
8: geneseq20056:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	86	4 AAB70146	Aab70146 Human G p
2	498	100.0	86	5 AAB76801	Abb76801 Human ZAQ
3	498	100.0	86	5 ABO10538	Abj0538 Human ZAQ
4	498	100.0	86	5 AAO15529	AAO15529 Human phy
5	498	100.0	86	5 AAB06306	Abb06306 Human G p
6	498	100.0	86	5 AAE24383	Aae24383 Human pro
7	498	100.0	86	7 ADD69104	Add69104 Human ZAQ
8	498	100.0	86	7 AD005360	Ado05360 Human pro
9	498	100.0	86	8 ADNA3256	Adn43256 Amino aci
10	498	100.0	86	8 ADRA2403	Adr24003 Human ZAQ
11	498	100.0	87	5 AAE24395	Aae24395 Human pro
12	498	100.0	89	5 AAE24392	Aae24392 Human pro
13	498	100.0	105	5 AAY66745	Aay66745 Membrane-
14	498	100.0	105	3 AAB18453	Aab18453 A human T
15	498	100.0	105	4 AAB70148	Aab70148 Human G p
16	498	100.0	105	4 AAB68427	Aab68427 Amino aci
17	498	100.0	105	4 AAU12406	Aau12406 Human PRO
18	498	100.0	105	4 AAB53096	Aab53096 Human ang
19	498	100.0	105	4 AAB52658	Aab52658 Human PRO
20	498	100.0	105	4 AAB48175	Aab48175 Human PRO
21	498	100.0	105	4 AAB48067	Aab48067 Human ext
22	498	100.0	105	5 AAM50773	Aam50773 Endocrine
23	498	100.0	105	5 AAU83674	Aau83674 Human PRO
24	498	100.0	105	5 AAB84902	Abb84902 Human PRO
25	498	100.0	105	5 AAO15527	Aao15527 Human phy

26	498	100.0	105	5 ABB06308	Abb06308 Human G p
27	498	100.0	105	5 AAE24382	Aae24382 Human pro
28	498	100.0	105	5 ABB95508	Abb95508 Human ang
29	498	100.0	105	6 ABUS8083	Abu58083 Human PRO
30	498	100.0	105	6 ABUS9161	Abu59161 Novel hum
31	498	100.0	105	6 ABUS8257	Abu82573 Human sec
32	498	100.0	105	6 ABO17850	AbO17850 Novel hum
33	498	100.0	105	6 ABUS0592	Abu05922 Human sec
34	498	100.0	105	6 ABUS0821	Abu0821 Human PRO
35	498	100.0	105	6 ABO33787	AbO33787 Novel hum
36	498	100.0	105	6 ABU13974	Abu13974 Human PRO
37	498	100.0	105	6 ABUS0880	Abu0880 Human end
38	498	100.0	105	6 ABUS0810	Abu08104 Human PRO
39	498	100.0	105	6 ABUS0763	Abu07603 Human ZVE
40	498	100.0	105	6 ABUS7255	Abu72559 Novel hum
41	498	100.0	105	6 ABUS6680	Abu66804 Human PRO
42	498	100.0	105	6 ABUS9885	Abu59885 Novel sec
43	498	100.0	105	6 ABUS9308	Abu59308 Human sec
44	498	100.0	105	6 ABUS9308	Abu59308 Human sec
45	498	100.0	105	6 ABO26005	AbO26005 Human PRO
46	498	100.0	105	6 ABO25075	AbO25075 Human sec
47	498	100.0	105	6 ABUS8213	Abu82130 Novel hum
48	498	100.0	105	6 ABUS9014	Abu59014 Human sec
49	498	100.0	105	6 ABUS9232	Abu59232 Novel hum
50	498	100.0	105	6 ABUS9457	Abu59457 Novel hum
51	498	100.0	105	6 ABUS9457	Abu59457 Novel hum
52	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
53	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
54	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
55	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
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65	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
66	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
67	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
68	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
69	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
70	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
71	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
72	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
73	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
74	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
75	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
76	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
77	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
78	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
79	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
80	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
81	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
82	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
83	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
84	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
85	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
86	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
87	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
88	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
89	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
90	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
91	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
92	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
93	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
94	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
95	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
96	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
97	498	100.0	105	6 ABUS9223	Abu92223 Novel hum
98	498	100.0	105	6 ABUS9223	Abu92223 Novel hum

99	498	100.0	105	6	ADB26915	ADB26915	Human	PRO	172	498	100.0	105	7	ADC49115	ADC49115	Novel	hum
100	498	100.0	105	6	ADB31202	ADB31202	Human	PRO	173	498	100.0	105	7	ADC49632	ADC49632	Novel	hum
101	498	100.0	105	6	AB72438	AB72438	Human	PRO	174	498	100.0	105	7	ADC47493	ADC47493	Novel	hum
102	498	100.0	105	6	ADA92933	ADA92933	Human	sec	175	498	100.0	105	7	ADC33044	ADC33044	Novel	hum
103	498	100.0	105	6	ADA61130	ADA61130	Homo sapi		176	498	100.0	105	7	ADC57398	ADC57398	Novel	hum
104	498	100.0	105	6	ADB24277	ADB24277	Human	PRO	177	498	100.0	105	7	ADC60589	ADC60589	Novel	hum
105	498	100.0	105	6	ADA96606	ADA96606	Human	PRO	178	498	100.0	105	7	ADC51064	ADC51064	Novel	hum
106	498	100.0	105	6	ADA81178	ADA81178	Human	PRO	179	498	100.0	105	7	ADC65591	ADC65591	Novel	hum
107	498	100.0	105	6	ADA96054	ADA96054	Human	PRO	180	498	100.0	105	7	ADC54689	ADC54689	Novel	hum
108	498	100.0	105	6	ADB26363	ADB26363	Human	PRO	181	498	100.0	105	7	ADC53650	ADC53650	Novel	hum
109	498	100.0	105	6	ADB21848	ADB21848	Human	PRO	182	498	100.0	105	7	ADC59173	ADC59173	Novel	hum
110	498	100.0	105	6	ABO34333	ABO34333	Human	sec	183	498	100.0	105	7	ADC56051	ADC56051	Novel	hum
111	498	100.0	105	7	ADA77627	ADA77627	Human	PRO	184	498	100.0	105	7	ADC58621	ADC58621	Novel	hum
112	498	100.0	105	7	ADB18367	ADB18367	Human	PRO	185	498	100.0	105	7	ADC14671	ADC14671	Novel	hum
113	498	100.0	105	7	ADA87050	ADA87050	Novel	hum	186	498	100.0	105	7	ADC47238	ADC47238	Novel	hum
114	498	100.0	105	7	ADA88153	ADA88153	Novel	hum	187	498	100.0	105	7	ADD08203	ADD08203	Novel	hum
115	498	100.0	105	7	ADA46541	ADA46541	Novel	hum	188	498	100.0	105	7	ADD03295	ADD03295	Novel	hum
116	498	100.0	105	7	ADB28571	ADB28571	Human	PRO	189	498	100.0	105	7	ADC90287	ADC90287	Novel	hum
117	498	100.0	105	7	ADB29123	ADB29123	Human	PRO	190	498	100.0	105	7	ADC82028	ADC82028	Human	PRO
118	498	100.0	105	7	ABO53220	ABO53220	Human	sec	191	498	100.0	105	7	ADC69706	ADC69706	Human	PRO
119	498	100.0	105	7	ADA77075	ADA77075	Human	PRO	192	498	100.0	105	7	ADC48595	ADC48595	Human	PRO
120	498	100.0	105	7	ADA22494	ADA22494	Human	sec	193	498	100.0	105	7	ADD10124	ADD10124	Human	PRO
121	498	100.0	105	7	ADA88705	ADA88705	Novel	hum	194	498	100.0	105	7	ADD07670	ADD07670	Novel	hum
122	498	100.0	105	7	ADA97710	ADA97710	Human	PRO	195	498	100.0	105	7	ADC78113	ADC78113	Novel	hum
123	498	100.0	105	7	ADB27467	ADB27467	Human	PRO	196	498	100.0	105	7	ADD04699	ADD04699	Novel	hum
124	498	100.0	105	7	ADB22400	ADB22400	Novel	hum	197	498	100.0	105	7	ADC82561	ADC82561	Novel	hum
125	498	100.0	105	7	ABO22590	ABO22590	Novel	hum	198	498	100.0	105	7	ADD06348	ADD06348	Novel	hum
126	498	100.0	105	7	ADA06660	ADA06660	Human	sec	199	498	100.0	105	7	ADC80655	ADC80655	Novel	hum
127	498	100.0	105	7	ABU72140	ABU72140	Human	mem	200	498	100.0	105	7	ADD11162	ADD11162	Human	PRO
128	498	100.0	105	7	ADA39353	ADA39353	Human	sec	201	498	100.0	105	7	ADD10461	ADD10461	Human	sec
129	498	100.0	105	7	ADA67091	ADA67091	Human	PRO	202	498	100.0	105	7	ADC48043	ADC48043	Human	PRO
130	498	100.0	105	7	ADB22952	ADB22952	Human	PRO	203	498	100.0	105	7	ADD08741	ADD08741	Novel	hum
131	498	100.0	105	7	ADB23725	ADB23725	Human	PRO	204	498	100.0	105	7	ADC77867	ADC77867	Novel	hum
132	498	100.0	105	7	ADA92447	ADA92447	Novel	hum	205	498	100.0	105	7	ADC80103	ADC80103	Novel	hum
133	498	100.0	105	7	ADB15510	ADB15510	Human	PRO	206	498	100.0	105	7	ADD06990	ADD06990	Novel	hum
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136	498	100.0	105	7	ADB73303	ADB73303	Novel	hum	209	498	100.0	105	7	ADC83237	ADC83237	Human	PRO
137	498	100.0	105	7	ADB38762	ADB38762	Novel	hum	210	498	100.0	105	7	ADD50830	ADD50830	Novel	hum
138	498	100.0	105	7	ADB96379	ADB96379	Human	PRO	211	498	100.0	105	7	ADD41285	ADD41285	Novel	hum
139	498	100.0	105	7	ADB78385	ADB78385	Novel	hum	212	498	100.0	105	7	ADD52424	ADD52424	Human	PRO
140	498	100.0	105	7	ADB38210	ADB38210	Novel	hum	213	498	100.0	105	7	ADD51076	ADD51076	Novel	hum
141	498	100.0	105	7	ADB66682	ADB66682	Novel	hum	214	498	100.0	105	7	ADD53164	ADD53164	Human	PRO
142	498	100.0	105	7	ADB85033	ADB85033	Human	PRO	215	498	100.0	105	7	ADD53716	ADD53716	Novel	hum
143	498	100.0	105	7	ADB89762	ADB89762	Human	PRO	216	498	100.0	105	7	ADD55344	ADD55344	Human	PRO
144	498	100.0	105	7	ADB90494	ADB90494	Human	PRO	217	498	100.0	105	7	ADD69106	ADD69106	Human	PRO
145	498	100.0	105	7	ADB39595	ADB39595	Novel	hum	218	498	100.0	105	7	ADD37214	ADD37214	Human	sec
146	498	100.0	105	7	ADB78139	ADB78139	Novel	hum	219	498	100.0	105	7	ADD56302	ADD56302	Human	PRO
147	498	100.0	105	7	ADB87205	ADB87205	Human	PRO	220	498	100.0	105	7	ADD51872	ADD51872	Human	PRO
148	498	100.0	105	7	ADB84787	ADB84787	Human	PRO	221	498	100.0	105	7	ADD02671	ADD02671	Human	PRO
149	498	100.0	105	7	ADB47218	ADB47218	Novel	hum	222	498	100.0	105	7	ADD50557	ADD50557	Human	PRO
150	498	100.0	105	7	ADB83902	ADB83902	Novel	hum	223	498	100.0	105	7	ADD02105	ADD02105	Human	PRO
151	498	100.0	105	7	ADB86825	ADB86825	Human	PRO	224	498	100.0	105	7	ADD54287	ADD54287	Novel	hum
152	498	100.0	105	7	ADB73057	ADB73057	Novel	hum	225	498	100.0	105	7	ADD54740	ADD54740	Human	PRO
153	498	100.0	105	7	ADB77430	ADB77430	Novel	hum	226	498	100.0	105	7	ADD50311	ADD50311	Human	PRO
154	498	100.0	105	7	ADB34587	ADB34587	Human	PRO	227	498	100.0	105	7	ADD51332	ADD51332	Novel	hum
155	498	100.0	105	7	ADB35691	ADB35691	Human	PRO	228	498	100.0	105	7	ADD92604	ADD92604	Human	PRO
156	498	100.0	105	7	ADB34035	ADB34035	Human	PRO	229	498	100.0	105	7	ADD91500	ADD91500	Human	PRO
157	498	100.0	105	7	ADB35139	ADB35139	Human	PRO	230	498	100.0	105	7	ADD04114	ADD04114	Human	PRO
158	498	100.0	105	7	ADB36243	ADB36243	Human	PRO	231	498	100.0	105	7	ADD26894	ADD26894	Novel	hum
159	498	100.0	105	7	ADB46638	ADB46638	Novel	hum	232	498	100.0	105	7	ADD32411	ADD32411	Novel	hum
160	498	100.0	105	7	ADC57851	ADC57851	Human	PRO	233	498	100.0	105	7	ADD22343	ADD22343	Human	PRO
161	498	100.0	105	7	ADC55215	ADC55215	Human	PRO	234	498	100.0	105	7	ADD79567	ADD79567	Human	PRO
162	498	100.0	105	7	ADC12082	ADC12082	Human	sec	235	498	100.0	105	7	ADD42103	ADD42103	Human	PRO
163	498	100.0	105	7	ADC56504	ADC56504	Human	PRO	236	498	100.0	105	7	ADD017920	ADD017920	Human	PRO
164	498	100.0	105	7	ADC07559	ADC07559	Human	sec	237	498	100.0	105	7	ADD92052	ADD92052	Human	PRO
165	498	100.0	105	7	ADC11549	ADC11549	Human	sec	238	498	100.0	105	7	ADD33515	ADD33515	Novel	hum
166	498	100.0	105	7	ADC36895	ADC36895	Human	PRO	239	498	100.0	105	7	ADD34067	ADD34067	Novel	hum
167	498	100.0	105	7	ADC21885	ADC21885	Human	PRO	240	498	100.0	105	7	ADD80119	ADD80119	Human	PRO
168	498	100.0	105	7	ADC50511	ADC50511	Novel	hum	241	498	100.0	105	7	ADD93156	ADD93156	Human	PRO
169	498	100.0	105	7	ADC72058	ADC72058	Novel	hum	242	498	100.0	105	7	ADD19576	ADD19576	Human	PRO
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245	498	100.0	105	7	ADD96009	AdD96009	Human	PRO	318	498	100.0	105	8	ADD77647	AdD77647	Novel	hum
246	498	100.0	105	7	ADDE2895	AdE2895	Human	PRO	319	498	100.0	105	8	ADD77893	AdD77893	Novel	hum
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248	498	100.0	105	7	ADDE26361	AdE26361	Novel	hum	321	498	100.0	105	8	ADD73983	AdD73983	Human	PRO
249	498	100.0	105	7	ADDE32963	AdE32963	Novel	hum	322	498	100.0	105	8	ADD774621	AdD774621	Human	PRO
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253	498	100.0	105	7	ADDE40993	AdE40993	Human	PRO	326	498	100.0	105	8	ADD74867	AdD74867	Human	PRO
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258	498	100.0	105	7	ADDE31620	AdE31620	Novel	hum	331	498	100.0	105	8	ADDE93463	AdE93463	Human	PRO
259	498	100.0	105	7	ADDE33261	AdE33261	Novel	hum	332	498	100.0	105	8	ADDE35044	AdE35044	Human	PRO
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266	498	100.0	105	7	ADDE95952	AdE95952	Novel	hum	339	498	100.0	105	8	ADDE92386	AdE92386	Human	PRO
267	498	100.0	105	7	ADDE95552	AdE95552	Human	PRO	340	498	100.0	105	8	ADDE922172	AdE922172	Novel	hum
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269	498	100.0	105	7	ADDE95120	AdE95120	Novel	hum	342	498	100.0	105	8	ADDE98148	AdE98148	Human	PRO
270	498	100.0	105	7	ADDE93619	AdE93619	Novel	hum	343	498	100.0	105	8	ADDE924365	AdE924365	Novel	hum
271	498	100.0	105	7	ADDE982033	AdE982033	Novel	hum	344	498	100.0	105	8	ADDE98719	AdE98719	Human	PRO
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275	498	100.0	105	7	ADDE982650	AdE982650	Novel	hum	348	498	100.0	105	8	ADDE905315	AdE905315	Human	PRO
276	498	100.0	105	7	ADDE916049	AdE916049	Novel	hum	349	498	100.0	105	8	ADDE919582	AdE919582	Human	PRO
277	498	100.0	105	7	ADDE916678	AdE916678	Novel	hum	350	498	100.0	105	8	ADDE911296	AdE911296	Novel	hum
278	498	100.0	105	7	ADDE915497	AdE915497	Novel	hum	351	498	100.0	105	8	ADDE913419	AdE913419	Human	PRO
279	498	100.0	105	7	ADDE914945	AdE914945	Novel	hum	352	498	100.0	105	8	ADDE908476	AdE908476	Novel	hum
280	498	100.0	105	8	ADDE948869	AdE948869	Novel	hum	353	498	100.0	105	8	ADDE915646	AdE915646	Human	PRO
281	498	100.0	105	8	ADDE91207	AdE91207	Novel	hum	354	498	100.0	105	8	ADDE912075	AdE912075	Novel	hum
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284	498	100.0	105	8	ADDE976655	AdE976655	Human	PRO	357	498	100.0	105	8	ADDE923813	AdE923813	Novel	hum
285	498	100.0	105	8	ADDE975113	AdE975113	Human	PRO	358	498	100.0	105	8	ADDE904102	AdE904102	Human	PRO
286	498	100.0	105	8	ADDE975859	AdE975859	Novel	hum	359	498	100.0	105	8	ADDE925003	AdE925003	Novel	hum
287	498	100.0	105	8	ADDE985091	AdE985091	Novel	hum	360	498	100.0	105	8	ADDE94632	AdE94632	Novel	hum
288	498	100.0	105	8	ADDE986917	AdE986917	Novel	hum	361	498	100.0	105	8	ADDE907300	AdE907300	Novel	hum
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294	498	100.0	105	8	ADDE973623	AdE973623	Human	PRO	367	498	100.0	105	8	ADDE982316	AdE982316	Human	PRO
295	498	100.0	105	8	ADDE975871	AdE975871	Human	PRO	368	498	100.0	105	8	ADDE97555	AdE97555	Novel	hum
296	498	100.0	105	8	ADDE978463	AdE978463	Novel	hum	369	498	100.0	105	8	ADDE957003	AdE957003	Novel	hum
297	498	100.0	105	8	ADDE941422	AdE941422	Human	sec	370	498	100.0	105	8	ADDE958599	AdE958599	Novel	hum
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308	498	100.0	105	8	ADDE924642	AdE924642	Human	PRO	381	498	100.0	105	8	ADDE952515	AdE952515	Novel	hum
309	498	100.0	105	8	ADDE974677	AdE974677	Human	PRO	382	498	100.0	105	8	ADDE954243	AdE954243	Novel	hum
310	498	100.0	105	8	ADDE905146	AdE905146	Human	PRO	383	498	100.0	105	8	ADDE981212	AdE981212	Human	PRO
311	498	100.0	105	8	ADDE975359	AdE975359	Human	PRO	384	498	100.0	105	8	ADDE956451	AdE956451	Novel	hum
312	498	100.0	105	8	ADDE976903	AdE976903	Novel	hum	385	498	100.0	105	8	ADDE912717	AdE912717	Novel	hum
313	498	100.0	105	8	ADDE986671	AdE986671	Novel	hum	386	498	100.0	105	8	ADDE911110	AdE911110	Human	sec
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315	498	100.0	105	8	ADDE978139	AdE978139	Novel	hum	388	498	100.0	105	8	ADDE920150	AdE920150	Human	sec
316	498	100.0	105	8	ADDE918472	AdE918472	Human	PRO	389	498	100.0	105	8	ADDE918650	AdE918650	Human	PRO
317	498	100.0	105	8	ADDE988781	AdE988781	Human	PRO	390	498	100.0	105	8	ADDE954795	AdE954795	Novel	hum

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391 498 100.0 105 8 ADG59835 Novel hum
392 498 100.0 105 8 ADH43605 Human PRO
393 498 100.0 105 8 ADG34162 Novel hum
394 498 100.0 105 8 ADI81259 Human PRO
395 498 100.0 105 8 ADI33632 Human PRO
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406 498 100.0 105 8 ADK82950 Human PRO
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412 498 100.0 105 8 ADM42558 Human PRO
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415 498 100.0 105 8 ADI95902 Human PRO
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417 498 100.0 105 8 ADK86960 Human Ege
418 498 100.0 125 8 ADS00464 Human EG-
419 498 100.0 125 8 ABJ05340 Target fu
420 498 100.0 130 5 ABJ05339 Human PTH

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ALIGNMENTS

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RESULT 1
AAB70146
ID AAB70146 standard; protein; 86 AA.
XX
AC AAB70146;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human G protein-coupled receptor protein-related sequence #2.
XX
KW Human; G protein-coupled receptor protein; nocitropic; neuroprotective;
KW hypotensive; orexigenic; anti-allergic; anti-anginal; antimicrobial;
KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
KW allergy; angina pectoris; infection; MRSA;
KW multiple resistant Staphylococcus aureus.
XX
OS Homo sapiens.
XX
PN WO200116309-A1.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP005685.
XX
PR 27-AUG-1999; 99JP-00241531.
PR 18-JUL-2000; 2000JP-00217474.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
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PI Watanabe T, Terao Y, Shintani Y;
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DR WPI; 2001-226684/23.
XX
PT New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
PT hypertension and anorexia.
XX

```

```

PS Example 4; Fig 9; 11pp; Japanese.
XX
CC The present sequence is provided in a specification relating to a protein
CC or its salt with an amino acid sequence identical or substantially
CC similar to a fully defined sequence of 393 amino acids as given in the
CC specification. The protein is useful in gene diagnosis and development of
CC preventives and remedies for diseases associated with dysfunction of the
CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
CC angina pectoris and infections (e.g. multiple resistant Staphylococcus
CC aureus. The proteins and DNA encoding the proteins are also useful for
CC the treatment of these diseases by gene therapy
XX
SQ Sequence 86 AA:

```

```

Query Match 100.0%; Score 496; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AVITGACERDVOCAGTCCATSLMLRGLRMCPTLGRGEGCHPSHKVPPFRKKHTCP 60
1 AVITGACERDVOCAGTCCATSLMLRGLRMCPTLGRGEGCHPSHKVPPFRKKHTCP 60
Db 1 AVITGACERDVOCAGTCCATSLMLRGLRMCPTLGRGEGCHPSHKVPPFRKKHTCP 60
QY 61 CLPNLLCSRPDPGRYRCMSMDLKNINF 86
61 CLPNLLCSRPDPGRYRCMSMDLKNINF 86
Db 61 CLPNLLCSRPDPGRYRCMSMDLKNINF 86

```

```

RESULT 2
AAB76801
ID AAB76801 standard; protein; 86 AA.
XX
AC AAB76801;
XX
DT 19-JUN-2002 (first entry)
XX
DE Human ZAG-1.
XX
KW Recombinant protein production; drug; reagent; food stuff.
XX
OS Homo sapiens.
XX
PN WO200208417-A1.
XX
PD 31-JAN-2002.
XX
PF 25-JUL-2001; 2001WO-JP006392.
XX
PR 25-JUL-2000; 2000JP-00229064.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Ito T, Tanaka Y, Kondo M;
XX
DR WPI; 2002-179906/23.
XX
PT Production of recombinant proteins in prokaryotes or eukaryotes
PT particularly with target proteins obtainable through gene recombination
PT technique, for use as drugs, reagents, raw materials for industries and
PT feeding stuffs.
XX
PS Disclosure; Page 133; 137pp; Japanese.
XX
CC The present invention relates to a method for producing recombinant
CC proteins. The method comprises preparing a recombinant vector for
CC transforming a host cell before culturing the obtained transformant,
CC assaying expression of the reporter gene and confirming high expression
CC of the reporter gene. The recombinant proteins are useful as drugs,
CC reagents, raw materials for industries and feeding stuffs. Also, the
CC proteins are obtainable on large-scale production. The present sequence
CC was used to illustrate the invention
XX
SQ Sequence 86 AA:

```


Query Match 100.0%; Score 498; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 7.4e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHPGSHKVPFFPKRKHTCP 60
 DB 1 AVITGACERDVOCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHPGSHKVPFFPKRKHTCP 60

QY 61 CLPNILCSRFPDGRYRCSDMLKNINF 86
 DB 61 CLPNILCSRFPDGRYRCSDMLKNINF 86

RESULT 3

ID ABB05338 standard; protein; 86 AA.

AC ABB05338;

DT 08-NOV-2002 (first entry)

DE Human ZAQ protein ligand.

KM Target peptide production; fusion peptide; protease-susceptible linker;
 KM parathyroid hormone; PTH; high expression rate;
 KM pharmaceutical application.

OS Homo sapiens.

PN WO200236762-A1.

PD 10-MAY-2002.

PF 29-OCT-2001; 2001WO-JP009476.

PR 30-OCT-2000; 2000JP-00331170.

PT 27-JUN-2001; 2001JP-00195522.

PS (TAKE) TAKEDA CHEM IND LTD.

PI Yamada T, Suenaga M;

DR WPI; 2002-417275/44.

DR N-PSDB; ABB06826.

PT Production of target peptide comprises cleavage of fusion peptide with
 PT parathyroid hormone peptide for efficient manufacture of target peptide
 PT without the need to remove N-terminal methionine.

PS Claim 14; Page 16; 103pp; Japanese.

CC The invention comprises a method of producing a target peptide. The C-
 CC terminal end of the target peptide is fused via a protease-susceptible
 CC linker to parathyroid hormone (PTH) residues 1-34. The method of the
 CC invention is useful for the clean and efficient production of a target
 CC peptide at a high expression rate on an industrial scale without the need
 CC to remove the N-terminal methionine from the product. The peptides
 CC produced by the method of the invention are suitable for pharmaceutical
 CC and other uses. The present protein sequence was used in the invention

XX Sequence 86 AA;

Query Match 100.0%; Score 498; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 7.4e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHPGSHKVPFFPKRKHTCP 60
 DB 1 AVITGACERDVOCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHPGSHKVPFFPKRKHTCP 60

QY 61 CLPNILCSRFPDGRYRCSDMLKNINF 86
 DB 61 CLPNILCSRFPDGRYRCSDMLKNINF 86

RESULT 4

ID AAO15529 standard; protein; 86 AA.

AC AAO15529;

DT 24-OCT-2002 (first entry)

DE Human physiologically-active ZAQ ligand-related protein 4.

KM Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
 KM colitis; diarrhoea.

OS Homo sapiens.

PN WO200257443-A1.

PD 25-JUL-2002.

PF 21-JAN-2002; 2002WO-JP000378.

PR 22-JAN-2001; 2001JP-00013027.

PT 17-MAY-2001; 2001JP-00147759.

PS (TAKE) TAKEDA CHEM IND LTD.

PI Yamada T, Suenaga M, Nishimura O;

DR WPI; 2002-566801/60.

PT Industrial production of physiologically-active ZAQ ligand by expressing
 PT in transformant prokaryote and refolding in redox buffer, for use in
 PT preventing or treating digestive diseases e.g. colitis and diarrhoea.

PS Claim 2; Page 79; 93pp; Japanese.

CC The invention comprises a method for producing an active peptide that has
 CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
 CC method of the invention is useful for the production of a physiologically
 CC -active ZAQ ligand for use in preventing or treating digestive diseases
 CC (e.g. colitis and diarrhoea). The present amino acid sequence represents a
 CC human physiologically active ZAQ ligand-related protein

XX Sequence 86 AA;

Query Match 100.0%; Score 498; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 7.4e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHPGSHKVPFFPKRKHTCP 60
 DB 1 AVITGACERDVOCGAGTCCCAISLMLRGLRMCTPLRGEGEGCHPGSHKVPFFPKRKHTCP 60

QY 61 CLPNILCSRFPDGRYRCSDMLKNINF 86
 DB 61 CLPNILCSRFPDGRYRCSDMLKNINF 86

RESULT 5

ID ABB06306 standard; protein; 86 AA.

AC ABB06306;

DT 27-MAY-2002 (first entry)

DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:21.

KM G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
 KM ZAQ; antidiarrhetic; laxative; drug development; digestive disease;
 KM colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.

```
XX Homo sapiens.
OS
XX WO200206483-A1.
PN
XX 24-JAN-2002.
PD
XX 17-JUL-2001; 2001WO-JP006162.
PF
XX 18-JUL-2000; 2000JP-00217442.
PR
XX 02-FEB-2001; 2001JP-00026779.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
PI
XX Hiruma S;
XX
XX WPI; 2002-188546/24.
DR
XX N-PSDB; ABL49635.
XX
XX PT Physiologically-active peptides from cows milk, useful for developing
PT drugs to treat ZAO-mediated diseases, particularly digestive diseases
PT like colitis, diarrhea, constipation and poor-absorption syndrome, by
PT gene therapy.
XX
XX PS Claim 1; Fig 9; 191pp; Japanese.
XX
XX CC The present invention describes a peptide containing an amino acid
CC sequence (I) identical to or substantially similar to that of the
CC sequences in AB06305 or AB06306, or its salt. (I) has antidiarrhetic and
CC laxative activities. The peptides and encoding DNAs from the present
CC invention are useful for developing drugs to treat digestive diseases
CC like colitis, diarrhoea, constipation and poor-absorption syndrome,
CC including gene therapy. The physiologically-active cows milk-originated
CC peptides are applicable as a specific ligand of brain-originated orphan G
CC protein-coupled receptor protein ZAO. ABL49615 to AB040659 and AB06303
CC to AB06315 represent sequences used in the exemplification of the
CC present invention
XX
XX SQ Sequence 86 AA;
XX
XX Query Match 100.0%; Score 498; DB 5; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 7.4e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGECHGSHKVPFFRRKXHTCP 60
XX |||||||
XX DB 1 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGECHGSHKVPFFRRKXHTCP 60
XX |||||||
XX QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
XX |||||||
XX DB 61 CLPNLCSRPDPGRYRCMDLKNINF 86
XX |||||||
XX
XX RESULT 6
XX AAE24383
XX ID AAE24383 standard; protein; 86 AA.
XX
XX AC AAE24383;
XX
XX DT 04-OCT-2002 (first entry)
XX
XX DE Human prokineticin 1 mature protein.
XX
XX KW Human, prokineticin 1; gastrointestinal motility; intestinal cancer;
XX irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
XX diabetic gastroparesis; chronic constipation; malabsorptive disorder;
XX inflammatory bowel disorder; analgesic; infectious disease.
XX
XX OS Homo sapiens.
XX
XX XX WO200236625-A2.
XX
XX PN
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PD 10-MAY-2002.
XX
XX PF 01-NOV-2001; 2001WO-US047969.
XX
XX PR 03-NOV-2000; 2000US-0245882P.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX XX Zhou Q, Ehler FJ;
XX
XX DR WPI; 2002-479752/51.
XX
XX DR N-PSDB; AAD39321.
XX
XX PT New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving impaired
PT gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation.
XX
XX PS Claim 1; Page 79-80; 86pp; English.
XX
XX CC The invention relates to human prokineticin 1 and 2 polypeptides that
XX CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
XX CC molecules encoding such polypeptides. Polypeptides of the invention are
XX CC useful for treating disorders involving impaired gastrointestinal
XX CC motility. They are useful for stimulating gastrointestinal motility in
XX CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
XX CC operational ileus, chronic constipation and gastrointestinal reflux
XX CC disease. The prokineticin antagonists are useful for inhibiting
XX CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
XX CC disorder, inflammatory bowel disorders, infectious diseases and
XX CC intestinal cancers. The antagonists also act as analgesics. The present
XX CC sequence is human prokineticin 1 mature protein
XX
XX SQ Sequence 86 AA;
XX
XX Query Match 100.0%; Score 498; DB 5; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 7.4e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGECHGSHKVPFFRRKXHTCP 60
XX |||||||
XX DB 1 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGECHGSHKVPFFRRKXHTCP 60
XX |||||||
XX QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
XX |||||||
XX DB 61 CLPNLCSRPDPGRYRCMDLKNINF 86
XX |||||||
XX
XX RESULT 7
XX ADD69104
XX ID ADD69104 standard; protein; 86 AA.
XX
XX AC ADD69104;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE Human ZAO-related protein - SEQ ID 82.
XX
XX KW angiogenesis inhibitor; cytostatic; antiinflammatory; cancer;
XX ovarian disease; diabetic retinopathy; inflammatory; ZAO; Bv8; ISE;
XX human.
XX
XX OS Homo sapiens.
XX
XX XX WO2003066860-A1.
XX
XX PN 14-AUG-2003.
XX
XX PD 03-FEB-2003; 2003WO-JP001057.
XX
XX PF 04-FEB-2002; 2002JP-00027299.
XX
XX PR (TAKE ) TAKEDA CHEM IND LTD.
XX
XX PA
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XX Ohtaki T, Maeda Y, Takatsu Y;
XX
XX WPI; 2003-646310/61.
XX DR N-PSDB; ADD69110.
XX
XX Angiogenesis inhibitors for treatment and prevention of cancer, ovarian
XX diseases and inflammatory disease.
XX
XX Claim 1; SEQ ID NO 82; 308bp; Japanese.
XX
XX The invention relates to a novel angiogenesis inhibitor comprising a
XX compound that inhibits the activity of an amino acid sequence given in
XX the specification. Angiogenesis-related proteins Bv8, ZAQ and ISR were
XX utilised within the method of the invention. The molecules of the
XX invention demonstrate cytostatic and antiinflammatory activities whilst
XX the method may be useful for treatment and prevention of cancer, ovarian
XX diseases, diabetic retinopathy and inflammatory disease. The current
XX sequence is that of the human ZAQ-related protein of the invention.
XX
XX Sequence 86 AA;
SQ
Query Match          100.0%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATISLWRLGRLMCTPLRGEGEGCHPGSHKVPFFRKXKHHTCP 60
   |||||||
DB 1 AVITGACERDVCGAGTCCATISLWRLGRLMCTPLRGEGEGCHPGSHKVPFFRKXKHHTCP 60
   |||||||

QY 61 CLPNLLCSRFPPDGRYRCSDMLDKNINF 86
   |||||||
DB 61 CLPNLLCSRFPPDGRYRCSDMLDKNINF 86
   |||||||

RESULT 8
ADO05360
ID ADO05360 standard; protein; 86 AA.
XX
XX ADO05360;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human prokineticin 1 (PK1), SEQ ID NO:9.
DE
XX
XX Human; prokineticin 1; PK1; circadian rhythm; modulation; drug screening;
XX circadian rhythm disorder; non-24-hour sleep-wake syndrome;
XX rapid time-zone change syndrome; jetlag; work-shift syndrome;
XX delayed phase sleep syndrome; advanced sleep phase syndrome;
XX irregular sleep-wake pattern syndrome; decreased amplitude syndrome;
XX seasonal affective disorder; ultradian rhythm; daydreaming; urination;
XX hunger; infarctian rhythm; female sexual receptivity; CNS;
XX central nervous syndrome; PK2 receptor antagonist; PK2 receptor agonist.
XX
XX Homo sapiens.
OS
XX
XX WO2003088904-A2.
ID
XX
XX 30-OCT-2003.
PD
XX
XX 15-APR-2003; 2003WO-US011538.
PF
XX
XX 15-APR-2002; 2002US-0372836P.
PR
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Zhou Q, Bullock CM;
PI
XX
XX WPI; 2003-854028/79.
DR
XX
XX Screening for compounds for modulating circadian rhythm, for treating
XX seasonal disorders, comprises determining ability of prokineticin-2
XX receptor antagonist or agonist to modulate one or more circadian rhythm

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PT function indicia.
XX
XX Disclosure; SEQ ID NO 9; 164bp; English.
XX
XX The invention relates to a method of screening for a compound for its
XX ability to modulate circadian rhythm. The method involved determining the
XX ability of a prokineticin 2 (PK2) receptor agonist or antagonist to
XX modulate one or more indicia of circadian rhythm function. The compound
XX is identified as being a PK2 receptor agonist or antagonist by
XX determining its effect on a predetermined signal such as calcium
XX mobilisation produced by the interaction of PK2 and a receptor selected
XX from the PK2 receptor (e.g., ADO05353) or the PK1 receptor (e.g.,
XX ADO05355). The invention is based on the findings that PK2 expression in
XX the suprachiasmatic nucleus (SCN) oscillates in a circadian fashion, and
XX that PK2 receptor activation modulates circadian rhythm in rats. The
XX invention also relates to a method of modulating the circadian rhythm of
XX an animal by administration of a PK2 receptor antagonist or agonist; a
XX composition comprising a detectably labelled PK2 and an isolated mouse
XX PK2 receptor; nucleic acid constructs, vectors and host cells comprising
XX a PK2 gene promoter (ADO05365-ADO05369) operably linked to a heterologous
XX nucleotide sequence; use of such constructs to identify modulators of
XX circadian rhythm and for the light regulated expression of a nucleic acid
XX molecule in an animal; and oligonucleotides at least 17 bases in length
XX which are able to hybridise to the human PK2 promoter ADO05365. The
XX methods of the invention are useful for identifying compounds for
XX modulating circadian rhythm. Such modulators include PK2 receptor
XX antagonists which promote sleep, and PK2 receptor agonists which promote
XX alertness. The circadian rhythm modulators may be used in the treatment
XX of circadian rhythm disorders such as non-24-hour sleep-wake syndrome,
XX rapid time-zone change syndrome (jetlag), work-shift syndrome, delayed
XX phase sleep syndrome, advanced sleep phase syndrome, irregular sleep-wake
XX pattern syndrome, syndrome associated with decreased amplitude, and
XX seasonal affective disorder. They may also be used for modulating
XX biological rhythms with a periodicity of less than 24 hours (ultradian
XX rhythm) such as daydreaming, urination or hunger, or those with a
XX periodicity of more than 24 hours (infradian rhythm) such as sexual
XX receptivity (heat) in female animals. The present sequence represents
XX human PK1.
XX
XX Sequence 86 AA;
SQ
Query Match          100.0%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATISLWRLGRLMCTPLRGEGEGCHPGSHKVPFFRKXKHHTCP 60
   |||||||
DB 1 AVITGACERDVCGAGTCCATISLWRLGRLMCTPLRGEGEGCHPGSHKVPFFRKXKHHTCP 60
   |||||||

QY 61 CLPNLLCSRFPPDGRYRCSDMLDKNINF 86
   |||||||
DB 61 CLPNLLCSRFPPDGRYRCSDMLDKNINF 86
   |||||||

RESULT 9
ADN43256
ID ADN43256 standard; protein; 86 AA.
XX
XX ADN43256;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX Amino acid sequence of human prokineticin 1 (PK1).
DE
XX
XX neurogenesis; prokineticin receptor; PKR; neural stem; progenitor cell;
XX neural regeneration; Alzheimer's disease; Parkinson's disease;
XX neurodegenerative disease; prokineticin 1; PK1.
XX
XX Homo sapiens.
OS
XX
XX WO2004032851-A2.
ID
XX
XX 22-APR-2004.
PD

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XX 03-OCT-2003; 2003MO-US031626.
XX
XX
XX 04-OCT-2002; 2002US-0416202P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Zhou Q, Cheng MY;
XX WPI; 2004-340794/31.
XX
XX Identifying a compound that modulates neurogenesis comprises contacting a
XX neural stem or progenitor cell with a compound that modulates
XX prokineticin receptor signaling and determining its ability to modulate
XX neurogenesis.
XX
XX Claim 26; Fig 6B; 103pp; English.
XX
XX The specification describes a method for identifying a compound that
XX modulates neurogenesis. The method comprises providing a compound that
XX modulates prokineticin receptor (PKR) signaling, contacting a neural stem
XX or progenitor cell with the compound, and determining the ability of the
XX compound to modulate neurogenesis. The method is useful for modulating
XX neurogenesis or for identifying compounds that modulate neurogenesis.
XX These are used for both ex vivo or in vivo therapeutic applications where
XX neural regeneration is desirable, such as in Alzheimer's disease,
XX Parkinson's disease or other debilitating neurodegenerative diseases. The
XX present sequence represents human prokineticin 1 (PK1), which may be used
XX in the method of the invention to modulate neurogenesis.
XX
XX Sequence 86 AA;
XX
XX Query Match 100.0%; Score 498; DB 8; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 7.4e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AVITGACERDVQCGAGTCCAIISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKXHTCP 60
XX 1 AVITGACERDVQCGAGTCCAIISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKXHTCP 60
XX
XX 61 CLPNLCSRFPDGRYRCMDLNINF 86
XX 61 CLPNLCSRFPDGRYRCMDLNINF 86
XX
XX RESULT 10
XX ADR24003
XX ID ADR24003 standard; protein; 86 AA.
XX
XX ADR24003;
XX
XX 21-OCT-2004 (first entry)
XX
XX Human ZAQ-1 ligand protein #1.
XX
XX antiangiogenic; antialcoholic; antiarrhythmic; antiarteriosclerotic;
XX anticonvulsant; antidepressant; antidiabetic; anti-HIV; antitumor;
XX antiparkinsonian; cerebroprotective; cytosstatic; eating disorders;
XX endocrine; gastrointestinal; gynecological; hypnotic; hypotensive;
XX neuroleptic; neuroprotective; nootropic; ophthalmological; tranquilizer;
XX vasotrophic; vulnary; monoclonal antibody; human; ZAQ-1; ligand;
XX hybridoma cell; assay; diagnosis; endometrial cancer; endometriosis;
XX ovulation disorder; digestive disease; angiogenesis; pregnancy;
XX eating disorder; sleeping disorder; seasonal depression;
XX reproductive dysfunction; endocrine disease; senile dementia;
XX Alzheimer's disease; aging; cerebral circulatory disorder; head trauma;
XX spinal injury; epilepsy; anxiety; depression; schizophrenia; alcoholism;
XX Parkinson's disease; hypertension; arteriosclerosis; arrhythmia;
XX premenstrual disorder syndrome; glaucoma; AIDS; diabetes.
XX
XX Homo sapiens.
XX
XX WO2004065419-A1.
XX
XX

XX 05-AUG-2004.
XX
XX
XX 21-JAN-2004; 2004MO-JP000498.
XX
XX 22-JAN-2003; 2003JP-00014055.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Matsumoto H, Horikoshi Y, Masuda Y, Ohtaki T;
XX WPI; 2004-593431/57.
XX
XX New monoclonal antibody having high avidity to human ZAQ-1 polypeptide,
XX useful for preventing, treating or diagnosing diseases such as
XX endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS,
XX Parkinson's disease and diabetes.
XX
XX Claim 1; SEQ ID NO 1; 64pp; Japanese.
XX
XX The invention relates to a monoclonal antibody (I) having high avidity to
XX human ZAQ-1 ligand polypeptides, comprising either of two fully defined
XX sequences of 86 amino acids (S1). (I) is ZL1-107a or ZL1-234a produced
XX from hybridoma cells ZL1-107 FERM BP-8256 or ZL1-234 FERM BP-8257. (I) is
XX useful for carrying out assay of the polypeptide containing (S1) which
XX involves reacting (I) with the test-liquid containing the polypeptide or
XX its salt, and measuring the ratio of the polypeptide bound to (I). (I) is
XX useful as a diagnostic or therapeutic agent for diagnosis and/or
XX treatment of diseases such as endometrial cancer, endometriosis or
XX ovulation disorder, digestive diseases, diseases associated with
XX angiogenesis, diseases relating to pregnancy, eating disorder, sleeping
XX disorder, seasonal depression, reproductive dysfunction, endocrine
XX diseases, senile dementia, Alzheimer's disease, various disorders caused
XX by aging, cerebral circulatory disorder, head trauma, spinal injury,
XX epilepsy, anxiety, depression, manic depression, schizophrenia,
XX alcoholism, Parkinson's disease, hypertension, arteriosclerosis,
XX arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes,
XX etc. This sequence corresponds to a ZAQ-1 ligand used in the invention.
XX
XX Sequence 86 AA;
XX
XX Query Match 100.0%; Score 498; DB 8; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 7.4e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AVITGACERDVQCGAGTCCAIISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKXHTCP 60
XX 1 AVITGACERDVQCGAGTCCAIISLWRLGLRMCTPLGRGEGECPGSHKVPFFRRKXHTCP 60
XX
XX 61 CLPNLCSRFPDGRYRCMDLNINF 86
XX 61 CLPNLCSRFPDGRYRCMDLNINF 86
XX
XX RESULT 11
XX AAE24395
XX ID AAE24395 standard; protein; 87 AA.
XX
XX AAE24395;
XX
XX 04-OCT-2002 (first entry)
XX
XX Human prokineticin 1 mutant protein #4.
XX
XX Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
XX irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
XX diabetic gastroparesis; chronic constipation; malabsorptive disorder;
XX inflammatory bowel disorder; analgesic; infectious disease; mutant;
XX mutein.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX

```

PN WO200236625-A2.
XX
XX 10-MAY-2002.
PD
XX
XX 01-NOV-2001; 2001WO-US047969.
PF
XX
XX 03-NOV-2000; 2000US-0245882P.
PR
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Zhou Q, Ehler FJ;
PI
XX
XX WPI; 2002-479752/51.
DR
XX
XX New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving impaired
PT gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation.
XX
XX Example 1; Page 85-86; 86pp; English.
PS
XX The invention relates to human prokineticin 1 and 2 polypeptides that
CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
CC molecules encoding such polypeptides. Polypeptides of the invention are
CC useful for treating disorders involving impaired gastrointestinal
CC motility. They are useful for stimulating gastrointestinal motility in
CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
CC operational ileus, chronic constipation and gastrointestinal reflux
CC disease. The prokineticin antagonists are useful for inhibiting
CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
CC disorders, inflammatory bowel disorders, infectious diseases and
CC intestinal cancers. The antagonists also act as analgesics. The present
CC sequence is human prokineticin 1 mutant protein
SQ
XX Sequence 87 AA;
SQ
XX
XX Query Match 100.0%; Score 498; DB 5; Length 87;
XX Best Local Similarity 100.0%; Pred. No. 7.5e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVOCGAGTCCATSLMRLGRLMCTPLGRGEGECHPGSHKVPFRKRKHTCP 60
DB 2 AVITGACERDVOCGAGTCCATSLMRLGRLMCTPLGRGEGECHPGSHKVPFRKRKHTCP 61
QY 61 CLPNLCSRFPPGRRYRCSDMLKNINF 86
DB 62 CLPNLCSRFPPGRRYRCSDMLKNINF 87

```

RESULT 12

```

AAE24392
ID AAE24392 standard; protein; 89 AA.
XX
XX AAE24392;
AC
XX
XX 04-OCT-2002 (first entry)
DT
XX
XX Human prokineticin 1 mutant protein #1.
DE
XX
XX Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
KW diabetic gastroparesis; chronic constipation; malabsorptive disorder;
KW inflammatory bowel disorder; analgesic; infectious disease; mutant;
KW mutain.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200236625-A2.
PN
XX
XX 10-MAY-2002.
PD
XX
XX 01-NOV-2001; 2001WO-US047969.
PF

```

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XX
XX 03-NOV-2000; 2000US-0245882P.
PR
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Zhou Q, Ehler FJ;
PI
XX
XX WPI; 2002-479752/51.
DR
XX
XX New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving impaired
PT gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation.
XX
XX Example 1; Page 84; 86pp; English.
PS
XX The invention relates to human prokineticin 1 and 2 polypeptides that
CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
CC molecules encoding such polypeptides. Polypeptides of the invention are
CC useful for treating disorders involving impaired gastrointestinal
CC motility. They are useful for stimulating gastrointestinal motility in
CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
CC operational ileus, chronic constipation and gastrointestinal reflux
CC disease. The prokineticin antagonists are useful for inhibiting
CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
CC disorders, inflammatory bowel disorders, infectious diseases and
CC intestinal cancers. The antagonists also act as analgesics. The present
CC sequence is human prokineticin 1 mutant protein
SQ
XX Sequence 89 AA;
SQ
XX
XX Query Match 100.0%; Score 498; DB 5; Length 89;
XX Best Local Similarity 100.0%; Pred. No. 7.7e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVOCGAGTCCATSLMRLGRLMCTPLGRGEGECHPGSHKVPFRKRKHTCP 60
DB 4 AVITGACERDVOCGAGTCCATSLMRLGRLMCTPLGRGEGECHPGSHKVPFRKRKHTCP 63
QY 61 CLPNLCSRFPPGRRYRCSDMLKNINF 86
DB 64 CLPNLCSRFPPGRRYRCSDMLKNINF 89

```

RESULT 13

```

AAE6745
ID AAE6745 standard; protein; 105 AA.
XX
XX AAE6745;
AC
XX
XX 05-APR-2000 (first entry)
DT
XX
XX Membrane-bound protein PRO1186.
DE
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
OS
XX
XX WO963088-A2.
PN
XX
XX 09-DEC-1999.
PD
XX
XX 02-JUN-1999; 99WO-US012252.
PF
XX
XX 02-JUN-1999; 98US-0087607P.
PR
XX
XX 02-JUN-1999; 98US-0087609P.
PR
XX
XX 02-JUN-1999; 98US-0087759P.
PR
XX
XX 03-JUN-1998; 98US-0087827P.
PR
XX
XX 04-JUN-1998; 98US-0088021P.
PR
XX
XX 04-JUN-1998; 98US-0088025P.
PR
XX
XX 04-JUN-1998; 98US-0088028P.
PR
XX
XX 04-JUN-1998; 98US-0088029P.
PR

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PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-008900P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089949P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.

PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

(GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
Wood WI, Yuan J;

WPI; 2000-072863/06.

N-PDB; AAZ65091.

Membrane-bound proteins and related nucleotide sequences.

Claim 12; Fig 266; 822p; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, T1b ligands and various enzymes. The membrane-bound proteins and receptor

CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
 CC also be useful for the preparation of PRO polypeptides, especially by
 CC recombinant techniques

XX Sequence 105 AA;

Query Match 100.0%; Score 498; DB 3; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMRLMCTPLRGEGEGCHPGSHKVPFPRKXHTCP 60
 DB 20 AVITGACERDVCGAGTCCATSLMRLMCTPLRGEGEGCHPGSHKVPFPRKXHTCP 79
 QY 61 CLPNLCSRFPPDGRYRCGMDLNINP 86
 DB 80 CLPNLCSRFPPDGRYRCGMDLNINP 105

RESULT 14

AAB18453
 ID AAB18453 standard; protein; 105 AA.

XX AAB18453;

DT 15-JAN-2001 (first entry)

DE A human TANGO 266 polypeptide.

XX TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.

XX Homo sapiens.

OS Homo sapiens.

FT Peptide 1.19 Location/Qualifiers
 FT Protein /note="signal sequence"
 FT /note="mature protein"

XX MO200052022-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US005226.

XX 01-MAR-1999; 99US-0122458P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

XX WPI; 2000-579269/54.

XX N-PSDB; AAA75155.

XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,
 PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
 PT treating cancer.

PS Claim 8; Fig 14; 175pp; English.

XX The present sequence represents a human TANGO 266 polypeptide. The
 CC specification also describes TANGO 262, TANGO 216, TANGO 261, and TANGO
 CC 267. The TANGO polypeptides can be used to modulate cellular
 CC proliferation, modulate cellular differentiation and/or modulate cellular
 CC adhesion. The proteins can be used to treat any von Willebrand factor-
 CC associated disorder, regulate extracellular matrix structuring, cellular
 CC adhesion, and cell trafficking and/or migration, modulate cellular
 CC interactions, modulate cell adhesion in proliferative disorders, such as
 CC cancer, modulate the proliferation, differentiation, and/or function of
 CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,
 CC blood and hematopoietic associated diseases and disorders, atelectasis,
 CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to treat
 CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,
 CC brain herniation, iatrogenic disease, inflammation, bacterial and viral
 CC meningitis, Alzheimer's disease, cerebral toxoplasmosis, Parkinson's
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and
 CC encephalitis, and treat hepatic disorders

XX Sequence 105 AA;

Query Match 100.0%; Score 498; DB 3; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMRLMCTPLRGEGEGCHPGSHKVPFPRKXHTCP 60
 DB 20 AVITGACERDVCGAGTCCATSLMRLMCTPLRGEGEGCHPGSHKVPFPRKXHTCP 79
 QY 61 CLPNLCSRFPPDGRYRCGMDLNINP 86
 DB 80 CLPNLCSRFPPDGRYRCGMDLNINP 105

RESULT 15

AAB70148
 ID AAB70148 standard; protein; 105 AA.

XX AAB70148;

DT 29-MAY-2001 (first entry)

DE Human G protein-coupled receptor protein-related sequence #4.

XX Human; G protein-coupled receptor protein; nocitropic; neuroprotective;
 KW hypotensive; orexigenic; antiallergic; antidiagonal; antimicrobial;
 KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
 KW allergy; angina pectoris; infection; MRSA;
 KW multiple resistant Staphylococcus aureus.

XX Homo sapiens.

XX WO200116309-A1.

XX 08-MAR-2001.

XX 24-AUG-2000; 2000WO-JP005685.

XX 27-AUG-1999; 99JP-00241531.

XX 18-JUL-2000; 2000JP-00217474.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Watanabe T, Terao Y, Shintani Y;

XX WPI; 2001-226684/23.

PT New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
PT hypertension and anorexia.
XX
XX Example 4; Page 113, 119pp; Japanese.
XX
CC The present sequence is provided in a specification relating to a protein
CC or its salt with an amino acid sequence identical or substantially
CC similar to a fully defined sequence of 393 amino acids as given in the
CC specification. The protein is useful in gene diagnosis and development of
CC preventives and remedies for diseases associated with dysfunction of the
CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
CC angina pectoris and infections (e.g. multiple resistant Staphylococcus
CC aureus). The proteins and DNA encoding the proteins are also useful for
CC the treatment of these diseases by gene therapy
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No.9,1e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGREGECHPGSHKVPFRRKXHTCP 60
DB 20 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGREGECHPGSHKVPFRRKXHTCP 79
QY 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
DB 80 CLPNLLCSRFPDGRYRCMDLKNINF 105
RESULT 16
AAB68427
ID AAB68427 standard; protein; 105 AA.
XX
AC AAB68427;
XX
DT 23-JUL-2001 (first entry)
XX
DE Amino acid sequence of a human Zven2 polypeptide.
XX
XX Zven1; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing;
XX antitumour; antiinflammatory; necrosis; tissue growth; digestive enzyme;
XX cellular differentiation; gastrointestinal cell contractility;
XX gastrointestinal motility; inflammation; hypermotility; diarrhoea;
XX Crohn's disease.
XX
OS Homo sapiens.
XX
XX WO200136465-A2.
XX
XX 25-MAY-2001.
XX
XX 14-NOV-2000; 2000WO-US031278.
XX
XX 16-NOV-1999; 99US-00442164.
XX 25-FEB-2000; 2000US-00511879.
XX 19-APR-2000; 2000US-00552203.
XX 07-JUN-2000; 2000US-0210332P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Shepard PO, Bishop PD, Whitmore TE, Thompson PP;
XX WPI; 2001-355611/37.
XX DR N-PSDB; AAFB5427.
XX
XX Novel isolated Zven polypeptide useful for inhibiting proliferation of
XX tumor cells, for treating small cell cancer of lung, to promote wound
XX healing, and for treating Crohn's disease and diarrhea.
PS Claim 27; Page 4; 98pp; English.

XX
CC The present sequence represents a human Zven2 polypeptide. The
CC specification also describes Zven1. The Zven1 gene is present on
CC chromosome 3p21.1-3p14.3. The specification also describes Zven2. Zven
CC polynucleotides and polypeptides are useful in veterinary and human
CC therapeutics, for treating small cell cancer of the lung, to promote
CC wound healing, to prevent or to treat an adverse reaction of the skin to
CC a skin-sensitizing agent or a skin-irritating agent, to stimulate the
CC immune system of an immunocompromised individual, as antitumour agents,
CC as antiinflammatory agents, as agents to regulate regeneration or
CC remodeling of tissue, as agents to modulate necrosis or tissue growth
CC developmental arrest, to inhibit proliferation of tumour cells, cellular
CC differentiation and necrosis, to treat disorders associated with
CC gastrointestinal cell contractility, secretion of digestive enzymes and
CC acids, gastrointestinal motility, recruitment of digestive enzymes,
CC inflammation, and conditions associated with hypermotility such as
CC diarrhoea and Crohn's disease
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No.9,1e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGREGECHPGSHKVPFRRKXHTCP 60
DB 20 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGREGECHPGSHKVPFRRKXHTCP 79
QY 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
DB 80 CLPNLLCSRFPDGRYRCMDLKNINF 105
RESULT 17
AAU12406
ID AAU12406 standard; protein; 105 AA.
XX
AC AAU12406;
XX
DT 24-OCT-2001 (first entry)
XX
XX Human PRO1186 polypeptide sequence.
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
XX prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
XX ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX A-peptide; Factor VIIA; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200140466-A2.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US032678.
XX
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 09-DEC-1999; 99US-0170262P.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 20-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000MO-US004414.
 PR 24-FEB-2000; 2000MO-US004914.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000MO-US006319.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 20-MAR-2000; 2000MO-US007377.
 PR 21-MAR-2000; 2000MO-US007372.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 05-JUN-2000; 2000US-0209632P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 11-AUG-2000; 2000MO-US020710.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 10-NOV-2000; 2000MO-US030873.
 XX
 XX (GENENTECH INC.)
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR
 DR WPI; 2001-408281/43.
 XX N-PSDB; AAS21478.
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 XX breast, prostate, cervical.
 PS Claim 12; Fig 470; 813pp; English.
 XX
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 XX Sequence 105 AA;
 SQ
 Query Match 100.0%; Score 498; DB 4; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9,1e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18
 AAB53096
 ID: AAB53096 standard; protein; 105 AA.
 XX
 XX AAB53096;
 AC
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.
 XX
 XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 PN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 XX 05-JAN-2000; 2000MO-US000219.
 XX
 PF 08-MAR-1999; 99MO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99MO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99MO-US020111.
 PR 08-SEP-1999; 99MO-US020594.
 PR 15-SEP-1999; 99MO-US021090.
 PR 15-SEP-1999; 99MO-US021547.
 PR 05-OCT-1999; 99MO-US023089.
 PR 30-NOV-1999; 99MO-US028313.
 PR 30-NOV-1999; 99MO-US028409.
 PR 02-DEC-1999; 99MO-US028564.
 PR 02-DEC-1999; 99MO-US028565.
 XX
 XX (GENENTECH INC.)
 XX
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Maresca SA;
 PI Paoni NF, Picti RM, Watanabe CK, Williams PM, Wood WI;
 DR
 DR WPI; 2001-090793/10.
 XX N-PSDB; AAC97496.
 DR
 PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic
 PT disorders, such as atherosclerosis, wounds or cancer.
 XX
 XX Claim 69; Fig 66; 293pp; English.
 PS
 XX The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity, diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or

CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
 CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to screen
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals
 CC useful for the development and screening of potential therapeutic agents.
 CC The present sequence represents a PRO protein of the invention

CC Sequence 105 AA:

Query Match 100.0%; Score 498; DB 4; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECPGSHKVPFRKRRKHTCP 60
 DB 20 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECPGSHKVPFRKRRKHTCP 79
 QY 61 CLPNILCSRFPDGRYRCMSMDLKNINF 86
 DB 80 CLPNILCSRFPDGRYRCMSMDLKNINF 105

RESULT 19

AAB65268
 ID AAB65268 standard; protein; 105 AA.

AC AAB65268;

DT 02-APR-2001 (first entry)

DE Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.

KW Human; secreted and transmembrane protein; PRO; cytosolic; cell death;

KM cancer; chromosomal mapping; gene mapping; tissue typing;

OS Homo sapiens.

XX WO200073454-A1.

PN 07-DEC-2000.

PD 30-MAR-2000; 2000WO-US008439.

XX 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 07-JUL-1999; 99US-0143048P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145688P.

PR 28-JUL-1999; 99US-0146222P.

PR 17-AUG-1999; 99US-0149396P.

PR 15-SEP-1999; 99WO-US021090.

PR 08-OCT-1999; 99WO-US021547.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028313.

PR 16-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030911.

PR 05-JAN-2000; 2000WO-US000219.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005941.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.

XX (GENTH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gerber H, Gertlsten ME, Goddard A, Godowski PJ,
 PI Klagsbrun CJ, Gurney AL, Klagsbrun JF, Napier MA, Pan J, Paoni NF,
 PI Roy MA, Stewart TX, Tamas D, Watanabe CK, Williams PM, Wood WI,
 PI Zhang Z;

XX WPI; 2001-032160/04.

DR N-PSDB; AAF44237.

XX PRO polynucleotides used to produce polypeptides used to target bioactive

PT molecules such as toxins, radiolabels or antibodies, to specific cells,
 PT to cause targeted cell death.

PS Claim 12; Fig 266; 935PP; English.

XX The present invention describes human secreted and transmembrane PRO

CC proteins. The PRO proteins have cytosolic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
 CC AAB65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention

XX Sequence 105 AA:

Query Match 100.0%; Score 498; DB 4; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECPGSHKVPFRKRRKHTCP 60
 DB 20 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECPGSHKVPFRKRRKHTCP 79
 QY 61 CLPNILCSRFPDGRYRCMSMDLKNINF 86
 DB 80 CLPNILCSRFPDGRYRCMSMDLKNINF 105

RESULT 20

AAB48175

ID AAB48175 standard; protein; 105 AA.

AC AAB48175;

DT 02-APR-2001 (first entry)

DE Human PRO1186 polypeptide.

KW PRO1186; PRO184; neoplastic; cell growth; tumour; cancer; breast;
 KW ovarian; renal; colorectal; uterine; prostate; lung; melanoma;
 KW central nervous system; leukemia; antitumor; cytosolic.

OS Homo sapiens.

XX Key Location/Qualifiers

PH Peptide 1..19

FT /note= "signal sequence"

```
FT Protein 20. .105
FT /note="mature protein"
FT Modified-site 33. .39
FT /note="N-myristoylation site"
FT Modified-site 35. .41
FT /note="N-myristoylation site"
FT Modified-site 46. .52
FT /note="N-myristoylation site"
FT Modified-site 88. .95
FT /note="tyrosine kinase phosphorylation site"
PN WO200075327-A1.
PD 14-DEC-2000.
XX
XX
XX PF 24-FEB-2000; 2000MO-US004914.
XX
XX PR 02-JUN-1999; 99MO-US012252.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 05-JAN-2000; 2000MO-US000219.
XX
XX (GETH ) GENENTECH INC.
XX
XX PI Ashkenazi AJ, Hillan KJ, Napier MA, Watanabe CK, Wood WI;
XX WPI; 2001-071078/08.
XX DR N-PSDB; AAC84469.
XX
XX PT Compositions for inhibiting neoplastic cell growth and treating tumor, a
XX cancer, comprises novel PRO1186 or PRO184 polypeptides or its agonist.
XX
XX PS Claim 31; Fig 2; 104pp; English.
XX
CC The invention provides PRO1186 and PRO184 polypeptides that can be used
CC for the inhibition of neoplastic cell growth and for treating tumours.
CC The PRO polypeptides can be expressed by standard recombinant
CC methodology. The PRO polypeptides or their agonists are useful for
CC inhibition of neoplastic cell growth and for treating tumors, cancers
CC such as breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder or central nervous system cancers or melanoma and leukemia. The
CC present sequence represents the human PRO1186 polypeptide (encoding CDNA
CC clone ID: DNA60621-1516)
XX
SQ Sequence 105 AA:
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 9,1e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCATSLMLRGRLMCTPLRGEGEGCHGSHKVPFRKRKHTCP 60
DB 20 AVITGACERDVCGAGTCCATSLMLRGRLMCTPLRGEGEGCHGSHKVPFRKRKHTCP 79
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
DB 80 CLPNLLCSRFPPDGRYRCSDMLKNINF 105
RESULT 21
AAB48067
ID AAB48067 standard; protein; 105 AA.
XX
XX AAB48067;
XX
XX 19-MAR-2001 (first entry)
XX
XX Human extracellular signaling molecule (EXCS) (ID 2006548CD1).
XX
XX Extracellular signaling molecule; EXCS; anti-inflammatory; human;
XX immunosuppressive; cytostatic; neuroprotective; gastrointestinal;
XX virucide; antibacterial; anti-HIV; human immunodeficiency virus;
XX antiinfectility; cerebroprotective; nootropic; antitumor; antifungal;
XX anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
```

```
KM keratolytic; protozoacide; gene therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO200070049-A2.
XX
XX PD 23-NOV-2000.
XX
XX PF 19-MAY-2000; 2000MO-US013975.
XX
XX PR 19-MAY-1999; 99US-0134949P.
XX PR 15-JUL-1999; 99US-0144270P.
XX PR 30-JUL-1999; 99US-0146700P.
XX PR 04-OCT-1999; 99US-0157508P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX PI Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
XX Azimzal Y, Lu DAM, Patterson C;
XX WPI; 2001-025021/03.
XX DR N-PSDB; AAC84303.
XX
XX PT New human extracellular signaling nucleic acids and polypeptides useful
XX for diagnosing, treating and preventing infections and gastrointestinal,
XX neurological, reproductive, and autoimmune/inflammatory disorders.
XX
XX PS Claim 1; Page 89; 114pp; English.
XX
XX CC The invention provides human extracellular signaling molecules (EXCS) and
XX polynucleotides which identify and encode EXCS. EXCS can be expressed by
XX standard recombinant methodology. The amino acid and nucleic acid
XX sequences of EXCS are useful for diagnosing, treating and preventing
XX infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis),
XX neurological (e.g. epilepsy, ischemic cerebrovascular disease, stroke),
XX reproductive (infertility, ovulatory defects, endometriosis), autoimmune
XX /inflammatory (acneic keratosis, acquired immunodeficiency syndrome
XX (AIDS), Addison's disease), and cell proliferative disorders including
XX cancers (of the breast, adrenal gland, bone). They may also be used to
XX treat fatal familial insomnia, nutritional and metabolic diseases of the
XX nervous system, myopathies, mental disorders (anxiety, schizophrenia,
XX mood), as well as infections caused by parasites (malaria, leishmania,
XX trypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial
XX (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus,
XX blastomycetes, dermatophytes) agents. The nucleic acids, polypeptides,
XX antagonists, agonists, pharmaceutical compositions, and antibodies may
XX also be used for treating or preventing disorders associated with
XX increased or decreased expression or activity of EXCS. EXCS
XX polynucleotides may also be used to detect and quantify gene expression
XX in biopsied tissues in which expression of EXCS may be correlated with
XX the disease, to determine presence or excess expression of EXCS, to
XX monitor regulation of EXCS levels during therapeutic intervention, to
XX detect the presence of associated disorders, as targets in microarray, to
XX generate hybridization probes, and to detect differences in gene
XX CC sequences among normal, carrier or affected individuals. Antibodies may
XX also be used in diagnosing disorders, in monitoring patients being
XX CC treated with EXCS agonists, antagonists or inhibitors. Sequences AAB48057
XX -B48082 represent the EXCS of the invention
XX
SQ Sequence 105 AA:
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 9,1e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCATSLMLRGRLMCTPLRGEGEGCHGSHKVPFRKRKHTCP 60
DB 20 AVITGACERDVCGAGTCCATSLMLRGRLMCTPLRGEGEGCHGSHKVPFRKRKHTCP 79
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
DB 80 CLPNLLCSRFPPDGRYRCSDMLKNINF 105
```

RESULT 22
AA050773 standard; protein; 105 AA.
ID AA050773;
AC AA050773;
XX
XX 23-APR-2002 (first entry)
XX
DE Endocrine gland-derived vascular endothelial growth factor.
XX
KW Endocrine gland-derived vascular endothelial growth factor; EG-VEGF;
KW human; cell proliferation; cell migration; fenestration;
KW cell differentiation; angiogenesis; chemotaxis; endocrine; infertility;
KW fertility; polycystic ovary syndrome; ovarian cyst; cancer; cytostatic;
KW diagnosis; therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..105
FT /label= Mature_protein
FT Modified-site 33
FT /note= "N-myristoylated"
FT Modified-site 35
FT /note= "N-myristoylated"
FT Modified-site 46
FT /note= "N-myristoylated"
XX
XX W0200200711-A2.
XX
XX 03-JAN-2002.
XX
XX 22-JUN-2001; 2001WO-US020116.
XX
XX 23-JUN-2000; 2000US-0213637P.
XX 07-SEP-2000; 2000US-0230978P.
XX 01-DEC-2000; 2000WO-US032678.
XX
XX (GETH) GENENTECH INC.
XX
XX Ferrara N, Watanabe C, Wood WI;
XX
XX WPI: 2002-130882/17.
XX N-PSDB; ABA91567.
XX
XX New endocrine gland-vascular endothelial growth factor (EG-VEGF)
XX polypeptides, agonists and antagonists, useful for regulating fertility,
XX and for treating cancer of the reproductive organs, e.g. ovarian or
XX prostate cancer.
XX
XX Claim 12; Fig 2; 133pp; English.
XX
XX The present sequence is that of a novel, tissue-restricted, growth and
XX differentiation factor termed endocrine gland-derived vascular
XX endothelial growth factor (EG-VEGF). The sequence is predicted from the
XX open reading frame of a cDNA clone (see ABA91567) obtained from an
XX ovarian tissue library. EG-VEGF induces proliferation, migration and
XX fenestrations in capillary endothelial cells derived from endocrine
XX glands, but has no effect on a variety of other endothelial and non-
XX endothelial cell types tested. The EG-VEGF precursor has a predicted
XX mol. wt. of 11715 and a pI of 9.05. The mature protein (mol. wt. 8600) is
XX cysteine-rich and is predicted to consist of a series of short beta
XX strands with large connecting loops held together by disulfide bonds
XX resulting in a flat fold with finger-like projections that act as
XX interactive surfaces. 80% Homology and 63% identity is shown to venom
XX protein A (VPRA) of the black mamba snake, and 76% homology and 58%
XX identity to human protein Bv8. EG-VEGF nucleic acids and polypeptides, as
XX well as agonists and antagonists, can be used in the treatment of
XX conditions associated with hormone-producing tissue, especially ovarian,
XX testicular, cervical, adrenal, placental or prostate tissue. The

CC condition may be polycystic ovary syndrome, cancer, especially ovarian
CC cancer, testicular cancer, prostate cancer or uterine cancer, or ovarian
CC cyst (all claimed). Fertility can be regulated using an EG-VEGF
CC antagonist to inhibit follicle maturation or ovulation. Methods are
CC claimed for identifying compounds that modulate EG-VEGF activity,
CC especially the ability to induce phosphorylation of a kinase involved in
CC cell proliferation or survival, to induce chemotaxis, angiogenesis, or
CC cell differentiation, or to induce endothelial cell proliferation
XX
XX SQ Sequence 105 AA;
XX
XX Query Match 100.0%; Score 498; DB 5; Length 105;
XX Best Local Similarity 100.0%; Pred. No. 9, 1e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKHHKTC 60
XX |||||
XX 20 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGCHPGSHKVPFFRRKHHKTC 79
XX
XX Db 61 CLPNLCSRFPDGRYRCGMDLKNINF 86
XX |||||
XX 80 CLPNLCSRFPDGRYRCGMDLKNINF 105
XX
XX Db
XX
XX RESULT 23
XX AA083674
XX ID AA083674 standard; protein; 105 AA.
XX
XX AA083674;
XX
XX 08-MAY-2002 (first entry)
XX
XX DE Human PRO protein, Seq ID No 166.
XX
XX
XX Human, secreted protein, PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha.
XX
XX OS Homo sapiens.
XX
XX PN W0200208288-A2.
XX
XX PD 31-JAN-2002.
XX
XX PF 29-JUN-2001; 2001WO-US021066.
XX
XX PR 20-JUL-2000; 2000US-0219556P.
XX PR 25-JUL-2000; 2000US-0220585P.
XX PR 25-JUL-2000; 2000US-0220605P.
XX PR 25-JUL-2000; 2000US-0220607P.
XX PR 25-JUL-2000; 2000US-0220624P.
XX PR 25-JUL-2000; 2000US-0220638P.
XX PR 25-JUL-2000; 2000US-0220664P.
XX PR 25-JUL-2000; 2000US-0220666P.
XX PR 25-JUL-2000; 2000US-0220893P.
XX PR 28-JUL-2000; 2000WO-US020710.
XX PR 01-AUG-2000; 2000US-0222425P.
XX PR 22-AUG-2000; 2000US-0227133P.
XX PR 23-AUG-2000; 2000WO-US023522.
XX PR 24-AUG-2000; 2000WO-US023528.
XX PR 10-NOV-2000; 2000WO-US030873.
XX PR 28-NOV-2000; 2000US-025366P.
XX PR 01-DEC-2000; 2000WO-US032678.
XX PR 20-DEC-2000; 2000US-0074725P.
XX PR 20-DEC-2000; 2000WO-US034956.
XX PR 28-FEB-2001; 2001WO-US006520.
XX PR 01-MAR-2001; 2001WO-US006666.
XX PR 22-MAR-2001; 2001US-00816744.
XX PR 10-MAY-2001; 2001US-00854208.
XX PR 10-MAY-2001; 2001US-00854280.
XX PR 25-MAY-2001; 2001WO-US017092.
XX

PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,
 XX WPI; 2002-172001/22.
 DR N-PSDB; ABRK3618.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.
 XX
 PS Claim 11; Fig 166; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumors, especially lung
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
 CC liver tumor. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumor necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVITGACERDVOCAGCTCAISIMLRGLMCTPLGEGEGCHPGSHKVPFRRKRNHTP 60
 DB 20 AVITGACERDVOCAGCTCAISIMLRGLMCTPLGEGEGCHPGSHKVPFRRKRNHTCP 79
 QY 61 CLPNLLCSRFPPDGRYRCMSMDLNINF 86
 DB 80 CLPNLLCSRFPPDGRYRCMSMDLNINF 105
 RESULT 24
 ABB84902
 ID ABB84902 strand; protein; 105 AA.
 XX
 AC ABB84902;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO1186 protein sequence SEQ ID NO:172.
 XX
 XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 KW
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US019692.

XX
 PR 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-0064365P.
 PR 23-AUG-2000; 2000WO-US023352.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0249222P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00757609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR N-PSDB; ABL8157.
 XX
 DR One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 DR useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 DR infarction), endothelial or angiogenic disorders in a mammal.
 XX
 XX Claim 11; Fig 172; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytosolic,
 CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCAIISLWLRGLRMCTPLGRGESECHPGSHKVPFFRRKXKHTCP 60
 |||||
 Db 20 AVITGACERDVQCGAGTCCAIISLWLRGLRMCTPLGRGESECHPGSHKVPFFRRKXKHTCP 79
 |||||
 QY 61 CLPNLLCSRPDPGRYRCMDLKNINF 86
 |||||
 Db 80 CLPNLLCSRPDPGRYRCMDLKNINF 105
 |||||

RESULT 25

AA015527
 ID AA015527 standard; protein; 105 AA.

XX AA015527;

DT 24-OCT-2002 (first entry)

DE Human physiologically-active ZAQ ligand-related protein 3.

KM Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
 colitis; diarrhoea.

XX Homo sapiens.

PN WO200257443-A1.

PD 25-JUL-2002.

PE 21-JAN-2002; 2002WO-JP000378.

PR 22-JAN-2001; 2001JP-00013027.

PR 17-MAY-2001; 2001JP-00147759.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Yamada T, Suenaga M, Nishimura O;

DR WPI; 2002-566801/60.

PT Industrial production of physiologically-active ZAQ ligand by expressing
 in transformant prokaryote and refolding in redox buffer, for use in
 preventing or treating digestive diseases e.g. colitis and diarrhea.

PS Example 3; Page 76-77; 93pp; Japanese.

CC The invention comprises a method for producing an active peptide that has
 the same activity as a ZAQ ligand isolated from eukaryotic cells. The
 method of the invention is useful for the production of a physiologically
 -active ZAQ ligand for use in preventing or treating digestive diseases
 (e.g. colitis and diarrhea). The present amino acid sequence represents a
 human physiologically active ZAQ ligand-related protein

SQ Sequence 105 AA;

Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCAIISLWLRGLRMCTPLGRGESECHPGSHKVPFFRRKXKHTCP 60
 |||||
 Db 20 AVITGACERDVQCGAGTCCAIISLWLRGLRMCTPLGRGESECHPGSHKVPFFRRKXKHTCP 79
 |||||
 QY 61 CLPNLLCSRPDPGRYRCMDLKNINF 86
 |||||
 Db 80 CLPNLLCSRPDPGRYRCMDLKNINF 105
 |||||

Search completed: May 16, 2005, 08:17:48
 Job time : 179 secs

Query Match 17.8%; Score 88.5; DB 2; Length 640;
Best Local Similarity 31.6%; Pred. No. 0.11; Mismatches 24; Indels 23; Gaps 4;
Matches 24; Conservative 5;
Db 13 CGAGTCCATISIMLRGLMCTPLGREGGECHGSHKVPFFRRKRKHHTC---PCL 62
488 CTAGRC---WM---TCLPMMGSGGTWPMRPMTP-----SRTGACLPPTCCSMLR 533
Qy 71 -----PDGRYRCSM 79
Db 534 RMRCGMAPGGRRCSTL 549

RESULT 3
T09059
notch4 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T09059
R/Rosen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; SC
submitted to the EMBL Data Library, October 1997
A/Description: Sequence of the mouse major histocompatibility locus class III region.
A/Reference number: Z16543
A/Accession: T09059
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1964 <ROM>
A/Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:92564945; PID:92564947
C/Genetics:
A/Gene: notch4
A/Map position: 17
A/Intons: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
1679/3; 1729/1; 1761/3
C/Superfamily: notch protein; ankyrin repeat homology; EGF homology
C/Keywords: receptor; signal transduction
F/514-545/Domain: EGF homology <EGF>

Query Match 16.3%; Score 81; DB 2; Length 1964;
Best Local Similarity 30.4%; Pred. No. 1.8; Mismatches 22; Indels 26; Gaps 5;
Matches 24; Conservative 7;
Db 7 CERDVQ-----CGAGTCCATISIMLRGLMCTPLGREGGECHGSHKVPFFRRKRKH 57
188 CERDINCFLEPGPCPGSTCHMTL---GSYQCLCPVGGRPGQ-----KLRKG 233
Qy 58 TCP---CLPNLCSRFPG 73
Db 234 ACPGSCCLNGGTCLVPEG 252

RESULT 4
A56175
adhesive plaque protein MgfP2 precursor - Mediterranean mussel
C/Species: Mytilus galloprovincialis (Mediterranean mussel)
C/Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C/Accession: A56175
R/Rouze, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Biol. Chem. 270, 6698-6701, 1995
A/Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth facto
A/Reference number: A56175; MUID:95204464; PMID:7896812
A/Accession: A56175
A/Molecule type: mRNA
A/Residues: 1-473 <IMO>
A/Cross-references: UNIPROT:Q25464; GB:D43794; NID:5602767; PIDN:BAA07852.1; PID:dl00843
C/Keywords: duplication
F/1-17/Domain: signal sequence #status predicted <SIG>
F/387-419/Domain: EGF homology <EGF1>
F/429-460/Domain: EGF homology <EGF>
F/23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #

Query Match 15.6%; Score 77.5; DB 2; Length 473;
Best Local Similarity 31.2%; Pred. No. 1.2; Mismatches 23; Indels 19; Gaps 7;
Matches 24; Conservative 11;

Qy 7 CERDVQCGAGTCCATISIMLRGLMCTPLGREGGECH-PSGSHKVPFFRRKRKHHTC---PCL 62
Db 117 CERKNV--CSPNDC-----KNNGKCSPLGKTYGKCTCSGGYGP---RCEVHACKPNPK 165
Qy 63 PNILCSRFPGGR--YRC 77
Db 166 NKGRG--FPDGKTGYKC 180

RESULT 5
T31070
notch homolog - sea urchin (Lytechinus variegatus)
C/Species: Lytechinus variegatus (variegated urchin)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C/Accession: T31070
R/Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
A/Title: Identification and localization of a sea urchin Notch homologue: insights into
A/Reference number: Z20966; MUID:97454256; PMID:9310331
A/Accession: T31070
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2531 <SHE>
A/Cross-references: EMBL:AF000634; NID:92570350; PID:92570351; PIDN:AA82088.1
C/Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 15.1%; Score 75; DB 2; Length 2531;
Best Local Similarity 29.9%; Pred. No. 9.7; Mismatches 23; Conservative 8; Indels 14; Gaps 5;
Matches 23; Conservative 8;
Db 3 ITGACRVDVCGAGTCCATISIMLRGLMCTPLGREGGECHGSHKVPFFRRKRKHHTCP 60
120 VDNVCKLEBPCQNGGTRLTSLMDYBC-FCIP-ANTGENCTDNDHC-----SNP 168
Qy 61 CLPNLCSRFPGGRYRC 77
Db 169 CLNGAVCTSSSDG-YSC 184

RESULT 6
XLRU
collipase precursor (validated) - human
N/Alternate names: procollipase
C/Species: Homo sapiens (man)
C/Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C/Accession: A42568; A33949; A03163
R/Sims, H.F.; Lowe, M.E.
Biochemistry 31, 7120-7125, 1992
A/Title: The human collipase gene: isolation, chromosomal location, and tissue-specific
A/Reference number: A42568; MUID:92353041; PMID:1643046
A/Accession: A42568
A/Molecule type: DNA
A/Residues: 1-112 <SIM>
A/Cross-references: UNIPROT:P04118; GB:M95529; NID:9180842; PIDN:AA805818.1; PID:914836
A/Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBI:110580
R/Lowe, M.E.; Rosenblum, J.L.; McGwen, P.; Strauss, A.W.
Biochemistry 29, 823-828, 1990
A/Title: Cloning and characterization of the human collipase cDNA.
A/Reference number: A33949; MUID:90248429; PMID:2337598
A/Accession: A33949
A/Molecule type: mRNA
A/Residues: 1-112 <LOW>
A/Cross-references: GB:J02883; NID:9180885; PIDN:AA82054.1; PID:9180886
A/Note: evidence of partial N-glycosylation, possibly at Asn-43
R/Sternby, B.; Engstrom, A.; Hellman, U.; Viherthy, A.M.; Borgstrom, N.H.; Borgstrom, B.
Biochim. Biophys. Acta 784, 75-80, 1984
A/Title: The primary sequence of human pancreatic collipase.
A/Reference number: A90652; MUID:84104937; PMID:6691966
A/Accession: A03163
A/Molecule type: protein
A/Residues: 23-108 <STB>
C/Comment: Collipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 sto

se the enzyme is washed off by bile salts, which are known to have an inhibitory effect

C:Genetics:

A:Gene: GDB:CLPS

A:Cross-references: GDB:127277; OMIM:120105

A:Map position: 6pter-6p21.1

A:Introns: 28/3; 69/3

C:Superfamily: colipase

C:Keywords: lipid digestion; lipid hydrolysis; pancreas

F:18-22/Domain: signal sequence #status predicted <SIG>

F:23-108/Domain: amino-terminal propeptide #status predicted <APP>

F:109-112/Domain: carboxyl-terminal propeptide #status predicted <CPP>

F:34-104,40-56,44-80,45-76,66-86/Distal/Disulfide bonds: #status predicted

F:69,72,75,76/Binding site: micellar substrate (Lys, Tyr, Tyr, Tyr) #status predicted

Query Match 14.7%; Score 73; DB 1; Length 112;

Best Local Similarity 31.2%; Pred. No. 1;

Matches 25; Conservative 6; Mismatches 37; Indels 12; Gaps 5;

Qy 7 CERDVGCGAGTCGATSLWRLGRLMCTPLRGEGEGCHPGSHKVPFPRKRGHTCPCLPNLL 66

Db 34 CMMSAQC-KSNCCGHSAL-GLARCTSMASENSEC---SVKTLV---GIYKCPGCRGLT 85

Qy 67 CSRPDPGRYRCSDMLKNINF 86

Db 86 C-----EGDKTIVGSINTNF 101

RESULT 7

A5356 tumor necrosis factor receptor 2 precursor [validated] - human

N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A53556; A56475; A48416; A23666; B35010; I38094

R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K

Science 248, 1019-1023, 1990

A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

A:Reference number: A53556; MUID:90260659; PMID:2160731

A:Accession: A53556

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <SMI>

A:Cross-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA5929.1; PID:g189186

R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squitres,

Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990

A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur

A:Reference number: A56475; MUID:91045991; PMID:2172983

A:Accession: A56475

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-195, 'R', 197-461 <KOH>

A:Cross-references: GB:M55994; GB:M8549; NID:g339757; PIDN:AAA36755.1; PID:g339758

R:Demic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.

Cytokine 2, 231-237, 1990

A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,

A:Reference number: A48416; MUID:91370690; PMID:1966549

A:Accession: A48416

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 23-461 <DEM>

A:Cross-references: GB:S63368; NID:g235648; PIDN:AA819824.1; PID:g235649

A:Note: sequence extracted from NCBI backbone (NCBIN:65368, NCBI:P63371)

R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990

A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra

A:Reference number: A56007; MUID:90349572; PMID:2166946

A:Accession: A56007

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEU>

A:Cross-references: GB:M5857; NID:g339751; PIDN:AAA63262.1; PID:g339752

R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.

J. Biol. Chem. 265, 20131-20138, 1990

A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec

A:Reference number: A23666; MUID:91056048; PMID:2173696

A:Accession: A23666

A:Status: preliminary

A:Molecule type: protein

A:Residues: 23-40;65-69;136-141;300-306 <LOB>

R:Engelmann, H.; Novick, D.; Wallach, D.

J. Biol. Chem. 265, 1531-1536, 1990

A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence

A:Reference number: A5010; MUID:90110215; PMID:2153136

A:Accession: B35010

A:Status: preliminary

A:Molecule type: protein

A:Residues: 27-31 <ENG>

R:Kuhnert, P.; Kemper, O.; Wallach, D.

Gene 150, 381-386, 1994

A:Title: Cloning, sequencing and partial functional characterization of the 5' region of

A:Reference number: I38094; MUID:95121934; PMID:7821811

A:Accession: I38094

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-37 <RES>

A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701

C:Genetics:

A:Gene: GDB:TNFR2

A:Cross-references: GDB:125914; OMIM:191191

A:Map position: 1p36.2-1p36.2

A:Introns: 26/3

A:Note: the list of introns is incomplete

C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-116/Domain: signal sequence #status predicted <SIG>

F:40-76/Domain: NGF receptor repeat homology <NG1>

F:78-119/Domain: NGF receptor repeat homology <NG2>

F:120-162/Domain: NGF receptor repeat homology <NG3>

F:164-201/Domain: NGF receptor repeat homology <NG4>

F:262-279/Domain: transmembrane #status predicted <TMN>

F:280-461/Domain: intracellular #status predicted <INT>

F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.6%; Score 72.5; DB 1; Length 461;

Best Local Similarity 29.5%; Pred. No. 4;

Matches 26; Conservative 7; Mismatches 28; Indels 27; Gaps 5;

Qy 2 VTTGACERD---VOCGAGTCGATSLWRLGRLMCTPL-----GREGEE----- 40

Db 105 VETGACTREQRNICRCRGWCALSK-QEGCLCARLKKRCRGFGVAPGTETSDVCKP 163

Qy 41 CHPGSHKVPFPRKRGHTCPCLPNLLCS 68

Db 164 CAPGT-----FSNTTSYDTCGRPHQICN 186

RESULT 8

A39804 thrombospondin precursor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A39804

R:Lawler, J.; Duquette, M.; Ferro, P.

J. Biol. Chem. 265, 8039-8043, 1991

A:Title: Cloning and sequencing of chicken thrombospondin.

A:Reference number: A39804; MUID:91217026; PMID:2022631

A:Accession: A39804

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1178 <LAW>

A:Cross-references: UNIPROT:P35440; GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764

C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc

F:325-383/Domain: von Willebrand factor type C repeat homology <WVC>

F:386-437/Domain: thrombospondin type 1 repeat homology <THR1>

F/442-498/Domain: thrombospondin type 1 repeat homology <THR2>
F/499-555/Domain: thrombospondin type 1 repeat homology <THR3>
F/658-697/Domain: EGF homology <EGF>

Query Match

Best Local Similarity 14.4%; Score 71.5; DB 1; Length 1178;
Pred. No. 12;
Matches 27; Conservative 8; Mismatches 32; Indels 57; Gaps 5;

11 VQCGAGCCAIISLM-----LRGLMCTPLGEGEGECHKV-----PF----- 50

Db 457 VTCGVGNTIRLRNCSPIPMQMGKNVGVNGRETEKCEKAPCVNGQWPMSPMSACTVTC 516

QY 51 ---FRKR-----KHRT-----PCLPMLCSRPDPG 73

Db 517 GGGIRERSRLCNSPEPYGKPCVDTKQHMCKKRCPIIDGCLSNCFPAECNSYPDG 576

QY 74 RYRC 77

Db 577 SWSC 580

RESULT 9

T13954

MEGF6 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T13954
R/Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomic 51, 27-34, 1998
A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A/Reference number: Z14126; MUID:98360089; PMID:9693030

A/Accession: T13954
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-1574 <NA>

A/Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449293

A/Experimental source: strain Sprague-Dawley; brain
C/Genetics:

A/Gene: MEGF6

Query Match 14.4%; Score 71.5; DB 2; Length 1574;
Best Local Similarity 28.4%; Pred. No. 15;
Matches 23; Conservative 6; Mismatches 31; Indels 21; Gaps 4;

QY 3 ITGAC-----ERDVCGAGTCATSLMRLGRLMCTPLGRGEGECHKVPPFRKXKH 57

Db 758 VTGECCLPPEKTEGDCAD--CPGGRMGLCGQICPACCEGACGCP-----ETG 804

QY 58 TPCCLPMLCSRPDPGRYRCS 78

Db 805 TCCCLPFGVGRCPD--TCS 822

RESULT 10

T13576
hypothetical protein 52C10.5 - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T13576

R/Benos, P.
Submitted to the EMBL Data Library, February 1999

A/Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A/Reference number: Z17690
A/Accession: T13576

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-1854 <BEN>

A/Cross-references: UNIPROT:O96836; EMBL:AL035311; NID:e1373062; PID:e1373064; PIDN:CAA2

C/Genetics:
A/Cross-references: FlyBase:FBgn0026309
A/Introns: 4/3; 53/3; 209/3; 962/1; 1632/1; 1666/2; 1739/1; 1793/1
A/Note: EG:52C10.5

Query Match 14.4%; Score 71.5; DB 2; Length 1854;

Best Local Similarity 36.4%; Pred. No. 17;
Matches 20; Conservative 6; Mismatches 22; Indels 7; Gaps 3;

QY 37 EGEGECHKVPPFRKXKHHTCPCLPMLCSR-----PPDGRYRCSMDLKNINF 86

Db 228 KAKEVCYCSQKFTFTFR-RKH-CLGQIFCSKCNQVVGMIIRCGDLKVCNY 280

RESULT 11

I51909

colipase precursor - rat
N/Alternate names: procollipase
C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: I51909; A34623

R/Payne, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.
Am. J. Physiol. 266, G914-G921, 1994

A/Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA
A/Reference number: I51909; MUID:94262798; PMID:8203536

A/Accession: I51909
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-112 <PAY>

A/Cross-references: UNIPROT:P17084; GB:M58370; NID:g203504; PIDN:AAA20505.1; PID:g20350

R/Biochem. Biophys. Res. Commun. 167, 130-136, 1990
A/Title: Rat pancreatic colipase mRNA: nucleotide sequence of a cDNA clone and nutrition

A/Reference number: A34623; MUID:90179738; PMID:2129524

A/Accession: A34623
A/Status: preliminary

A/Molecule type: mRNA
A/Residues: 1-117, 'V', 19-112 <WTC>

A/Cross-references: GB:M33333; NID:g203502; PIDN:AAA0943.1; PID:g203503

C/Superfamily: colipase
C/Keywords: lipid digestion; lipid hydrolysis; pancreas

F/1-17/Domain: signal sequence #status predicted <SIG>
F/18-112/Product: colipase #status predicted <WAT>

Query Match 14.3%; Score 71; DB 2; Length 112;
Best Local Similarity 31.1%; Pred. No. 17;
Matches 19; Conservative 5; Mismatches 29; Indels 8; Gaps 3;

QY 7 CERDVCGAGTCATSLMRLGRLMCTPLGRGEGECHKVPPFRKXKHHTCPCLPML 66

Db 34 CANSQC-KSRCCQHTIL-GIARCTHKAMENSECPKILYIYR-----CPCRGLT 85

QY 67 C 67

Db 86 C 86

RESULT 12

S34665
collagen, cuticular - root-knot nematode (Meloidogyne incognita)

C/Species: Meloidogyne incognita
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S34665
R/van der Eycken, W.V.; de Almeida Engler, J.; van Montagu, M.; Ghysen, G.

Submitted to the EMBL Data Library, July 1993

A/Description: Identification and analysis of a cuticular collagen gene from the plant-i

A/Reference number: S34665
A/Accession: S34665

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-286 <VAN>

A/Cross-references: UNIPROT:Q25467; EMBL:Z24734; NID:g395144; PIDN:CAA80860.1; PID:g3951

Query Match 14.3%; Score 71; DB 2; Length 286;
Best Local Similarity 40.5%; Pred. No. 3.8;
Matches 15; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 33 PLGRGEGCHKVPPFRKXKHHTCPCLPMLCSR 69

Db 234 PSKRGAGGQEPHPPQPGQDAQYCCPPPSLSR 270

RESULT 13

GYHU

granulin precursor [validated] - human

N.Alternate names: epithelin

M.Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin F; gran

C.Species: Homo sapiens (man)

C.Date: 30-Sep-1992 #sequence_revision 03-May-1996 #text_change 09-Jul-2004

C.Accession: JCI284; A38128; A36698; B36698; D36698; A56873

R.Bhandari, V.; Bateman, A.

Biochem. Biophys. Res. Commun. 188, 57-63, 1992

A.Title: Structure and chromosomal location of the human granulin gene.

A.Reference number: JCI284; PMID:93038704; PMID:1417868

A.Molecule type: DNA

A.Residues: 1-593 <BNA>

A.Cross-references: UNIPROT:P28799; UNIPROT:Q9UC10

R.Ploman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J

U. Biol. Chem. 267, 13073-13078, 1992

A.Title: The epithelin precursor encodes two proteins with opposing activities on epithe

A.Reference number: A38128; PMID:92317004; PMID:1618805

A.Accession: A38128

A>Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-593 <PLO>

A.Cross-references: GB:X62320; NID:G31192; PIDN:CAA44196.1; PID:G31193

R.Bhandari, V.; Palfrey, R.G.E.; Bateman, A.

Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992

A.Title: Isolation and sequence of the granulin precursor cDNA from human bone marrow re

A.Reference number: A38118; PMID:92179253; PMID:1542665

A.Accession: A38118

A.Molecule type: mRNA

A.Residues: 1-406, 'R', 408-433, 'G', 435-453, 'G', 455-459, 'O', 461-546, 'A', 548-566, 'R', 568-59

A.Cross-references: GB:M75161; NID:G183612; PIDN:AAA58617.1; PID:G183613

R.Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, S.

Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990

A.Title: Granulins, a novel class of peptide from leukocytes.

A.Reference number: A36698; PMID:91097544; PMID:2268320

A.Accession: A36698

A.Molecule type: protein

A.Residues: 281-336 <BNT>

A.Note: this protein was purified and characterized as granulin A

A.Accession: B36698

A.Molecule type: protein

A.Residues: 206-218, 'H', 220-233 <BA2>

A.Note: this protein was purified and characterized as granulin B

A.Accession: C36698

A.Molecule type: protein

A.Residues: 364-367, 'X', 369-385, 'H', 387-396 <BA3>

A.Note: this protein was purified and characterized as granulin C

A.Accession: D36698

A.Molecule type: protein

A.Residues: 442-446, 'XDTSS', 456-458, 'DG' <BA4>

R.Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.

Br. J. Cancer 67, 686-692, 1993

A.Title: Characterisation of UGP and its relationship with beta-core fragment.

A.Reference number: A56873; PMID:93229246; PMID:8471426

A.Accession: A56873

A.Molecule type: protein

A.Residues: 281-283, 'X', 285-289, 'S', 291-295 <KAR>

A.Experimental source: urine

A.Note: sequence extracted from NCBI backbone (NCBI:P.129524)

C.Genetics:

A.Gene: GDB:GRN

A.Cross-references: GDB:136006; OMIM:139945

A.Map position: 17pter-17qter

A.Introns: 46/3; 86/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3

C:Superfamily: granulin

C:Keywords: glycoprotein; tandem repeat

F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-593/Product: granulin #status predicted <MAT>
F:18-593/Product: programulin #status predicted <PRO>
F:18-44/Product: paragranulin #status predicted <GR>
F:158-113/Product: granulin G #status predicted <GR>
F:123-179/Product: granulin F #status predicted <GR>
F:206-261/Product: granulin A #status experimental <GRA>
F:281-336/Product: granulin B #status experimental <GR>
F:364-417/Product: granulin C #status experimental <GR>
F:442-456/Product: granulin D #status predicted <GR>
F:518-573/Product: granulin E #status predicted <GR>
F:368/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 14.3% Score 71; DB 1; Length 593;

Best Local Similarity 24.2% Pred. No. 7.2; Indels 34; Gaps 5;

Matches 22; Conservative 6; Mismatches 29; Indels 34; Gaps 5;

QY 5 GACERDVOCAGTCCATSLMLRGLMCTPLGREGGCHPGSHKVPFRKRRKHTCPCLPN 64

Db 59 GPCQVDHAGSHGSCIFR-VSGTSSCCPF-PEAVACDGD-----HHCCP--RG 102

QY 65 LIGS-----RPPDGKRYRC 77

Db 103 FHCSADGRSCFORSNNNSVGAIQCPDSQFEC 133

RESULT 14

148141

acroggranin - guinea pig (fragment)

C.Species: Cavia porcellus (guinea pig)

C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C.Accession: I48141

R.Baba, T.; Hoff, H.B.

Mol. Reprod. Dev. 34, 233-243, 1993

A.Title: Acroggranin, an acrosomal cysteine-rich glycoprotein, is the precursor of the gro

A.Reference number: I48141; PMID:9328994; PMID:8471244

A.Accession: I48141

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-591 <RES>

A.Cross-references: UNIPROT:P28797; GB:M86735; NID:G191234; PIDN:AAA37030.1; PID:G191235

C:Superfamily: granulin

Query Match 14.2% Score 70.5; DB 2; Length 591;

Best Local Similarity 19.8% Pred. No. 8.1; Indels 53; Gaps 5;

Matches 24; Conservative 12; Mismatches 32; Indels 53; Gaps 5;

QY 7 CERDVOCAG-TCCATSLMLRGLMCTPLGR-----EGEGCHPGSH 46

Db 283 CDQVSCBEGQTCCLQ---SKMGCCPPKXAVCCEDHVNCCPERFRCHTEKDTCEQGL 339

QY 47 KVPFRK-----RKHTC---PCLPNLCSRFPPDGKRYR 76

Db 340 QVPMQKTPAPGSRPSPPGPPGPPSPGPRSEISCEDEVVSCRPNIICRLASGEWG 399

QY 77 C 77

Db 400 C 400

RESULT 15

T16840

hypothetical protein T10E10.4 - Caenorhabditis elegans

C.Species: Caenorhabditis elegans

C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C.Accession: T16840

R.Giesel, C.

submitted to the EMBL Data Library, October 1995

A.Description: The sequence of C. elegans cosmid T10E10.

A.Reference number: Z18588

A.Accession: T16840

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

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A:Residues: 1-1101 <GEI>
A:Cross-references: UNIPROT:Q22378; EMBL:U39644; NID:g1049339; P1D:g1049343; P1D:AAA803
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESB-T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 14.2%; Score 70.5; DB 2; Length 1101;
Best Local Similarity 22.9%; Pred. No. 14;
Matches 27; Conservative 6; Mismatches 36; Indels 49; Gaps 5;
QY 7 CERDVQCAAGTCCATSLWLRG-----LRMCTPLRR-- 36
Db 761 CPPGNQGENGVCCPMPWSSGSIASVCGMANSCPIGICRGRCGLEPLTLCNGBAS 820
QY 37 -----EGEECHGG-----SHKVFPRKRKHKHCPCILNLGSFPPGRGRCSM 79
Db 821 MRCYRGABCPFRGYGTCTPLGGCCCLSMSEVCTCRNSNAVCCSPNNVC--PGGA-SCTM 874

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Search completed: May 16, 2005, 06:35:40
Job time : 41 secs